

Query Match 67.0%; Score 13.4; DB 3; Length 67;
 Best Local Similarity 93.3%; Pred. No. 1.3e+05;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 AAAAGCTTCTTCAA 17
 |||||
 Db 64 AAAAGCTTCTTAA 50

RESULT 30

CG613923/c

LOCUS 68 bp mRNA linear GSS 02-OCT-2003
 DEFINITION OST301723 Mus musculus 129Sv/Ev Mus musculus CDNA clone OST301723,
 mRNA sequence.

ACCESSION CG613923
 VERSION CG613923.1 GI:37437772

KEYWORDS

SOURCE GSS.
 Mus musculus (house mouse)

ORGANISM

Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muridea; Muridae; Murinae; Mus.

REFERENCE

AUTHORS

1 (bases 1 to 68)
 Zambrowicz,B.P., Abuin,A., Ramirez-Solis,R., Richter,L.J.,
 Piggett,U., BeltrandelRio,H., Buxton,E.C., Edwards,J., Finch,R.A.,
 Fridde,C.J., Gupta,A., Hansen,G., Hu,Y., Huang,W., Jaing,C.,
 Key,B.W. Jr., Klipp,P., Konhauff,B., Ma,Z.-Q., Markesich,D.,
 Payne,R., Porter,D.G., Qian,N., Shaw,J., Schrick,J., Shi,Z.-Z.,
 Sparks,M.J., Van Sligtenhorst,I., Vogel,P., Walke,W., Xu,N.,
 Zhu,Q., Person,C. and Sands,A.T.
 Wnk1 kinase deficiency lowers blood pressure in mice: a gene-trap
 screen to identify potential targets for therapeutic intervention
 Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)

JOURNAL

PUBMED

14610273

COMMENT

Contact: Zambrowicz BP
 OmbiBank
 Lexicon Genetics Incorporated
 4000 Research Forest Drive, The Woodlands, TX 77381, USA
 Email: material@lexgen.com
 Gene trap sequence tag generated by 3' RACE from mouse ES cells as
 described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)
 Class: Gene trap.

FEATURES

source

Location/Qualifiers
 1..68
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="129Sv/Ev"
 /db_xref="taxon:10090"
 /clone="OST301723"
 /cell_type="embryonic stem cell"
 /clone_lib="Mus musculus 129Sv/Ev"

ORIGIN

Query Match 67.0%; Score 13.4; DB 10; Length 68;
 Best Local Similarity 93.3%; Pred. No. 1.3e+05;

Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATAAAGCTTCTTC 15
 |||||
 Db 18 ATAAAGCTTCTTC 4

Search completed: March 2, 2006, 01:14:25
 Job time : 2947 secs

ACCESSION Malus x domestica cDNA clone AAAA003533, mRNA sequence.
VERSION CN855909
KEYWORDS CN855909.1 GI:48111336
SOURCE EST.
ORGANISM Malus x domestica
Malus x domestica
Bakaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids I; Rosales; Rosaceae; Maloideae; Malus.
1 (bases 1 to 64)
REFERENCE Beuning, L., Bowen, J., Crowhurst, R., Glaeve, A., Jansen, B.,
AUTHORS Martiney, S., Newcomb, R., Ross, G., Snowden, K., Walton, E. and Yauk, Y.
TITLE HortResearch Apple EST Project
JOURNAL Unpublished (2004)
COMMENT Contact: Gleave, A.
The Horticulture and Food Research Institute of New Zealand Ltd
120 Mc Albert Rd, Mc Albert, Auckland, New Zealand
Tel: 00 64 09 815 4200
Fax: 00 64 09 815 4201
Email: est@hortresearch.co.nz.
Location/Qualifiers
FEATURES
source
1..64
/organism="Malus x domestica"
/mol_type="mRNA"
/db_xref="taxon:3750"
/clone="AAAA003533"
/rname_type="fruit"
/dev_stage="59 days after full bloom, seeds removed"
/clone_id="AAAA" Royal Gala 59 DAFB fruit, seeds
removed"
/note="Vector: PBK-CMV; Library sequenced by Genesis
Research & Development"

ORIGIN
Query Match 67.0%; Score 13.4; DB 7; Length 64;
Best Local Similarity 93.3%; Pred. No. 1.3e+05;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 2 TAAAAAGCTCTTCA 16
Db 64 TAAAAAGCTCTTCA 50

RESULT 28
AG222033/c
LOCUS AG222033 65 bp DNA linear GSS 19-JUL-2003
DEFINITION Lotus corniculatus var. japonicus DNA, clone:ljb06h23_r, genomic
survey sequence.
ACCESSION AG222033
VERSION AG222033.1 GI:26528885
KEYWORDS GSS.
SOURCE Lotus corniculatus var. japonicus (Lotus japonicus)
ORGANISM Lotus corniculatus var. japonicus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Loteeae;
Lotus.
1
REFERENCE Sato, S., Nakamura, Y. and Tabata, S.
AUTHORS Lotus japonicus BAC End sequences
JOURNAL Published Only in Database (2002)
REFERENCE 2 (bases 1 to 65)
AUTHORS Sato, S.
TITLE Direct Submission
JOURNAL Submitted (20-NOV-2002) Shusei Sato, Kazusa DNA Research Institute,
The First Laboratory for Plant Gene Research; 2-6-7
Kazusa-Kamatari, Kisarazu, Chiba 292-0818, Japan
FEATURES (E-mail: sato@kazusa.or.jp, URL: http://www.kazusa.or.jp/en/plant/,
source Tel: 81-438-52-3935 (ex. 2336), Fax: 81-438-52-3934)
1..65
Location/Qualifiers
/organism="Lotus corniculatus var. japonicus"

/mol_type="genomic DNA"
/strain="Miyakojima MG-20"
/variety="japonicus"
/db_xref="taxon:34305"
/clone="ljb06h23_r"
/clone_id="genomic BAC library"
/note="VECTOR: pBeloBAC11
synonym: Lotus japonicus"

ORIGIN
Query Match 67.0%; Score 13.4; DB 10; Length 65;
Best Local Similarity 93.3%; Pred. No. 1.3e+05;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 5 AAGCTTCTCAACA 19
Db 24 AAGCTTCTCAACA 10

RESULT 29
B1749485/c
LOCUS B1749485 67 bp mRNA linear EST 25-SEP-2001
DEFINITION ro78f09.y1 Heterodera glycines J2 PAMPI v8 Chiapelli; McCarter
Heterodera glycines cDNA 5', mRNA sequence.
ACCESSION B1749485
VERSION B1749485.1 GI:15771287
KEYWORDS EST.
SOURCE Heterodera glycines
ORGANISM Heterodera glycines
Eukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina;
Tylenchoidea; Heterodera; Heteroderidae; Heteroderinae; Heterodera.
1 (bases 1 to 67)
REFERENCE McCarter, J., Clifton, S., Chiapelli, B., Pope, D., Martin, J.,
AUTHORS Wylie, T., Dante, M., Marra, M., Hillier, L., Kucaba, T., Theising, B.,
Bowers, Y., Gildoms, M., Ritter, E., Bennett, J., Franklin, C.,
Tsagaris, S., Ronko, I., Kennedy, S., Maguire, L., Beck, C.,
Underwood, K., Steptoe, M., Allen, M., Person, B., Swaller, T.,
Harvey, N., Schurk, R., Kohn, S., Shin, T., Jackson, Y., Cardenas, M.,
McCann, R., Waterson, R. and Wilson, R.
The Washington Univ. Nematode EST Project, 1999
Unpublished (1999)
CONTACT McCarter JP
The Washington Univ. Nematode EST Project, 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
The library was constructed by Brandi Chiapelli and Dr. James
McCarter (bchiapell@watson.wustl.edu & jmcarter@watson.wustl.edu) at
Washington University, St. Louis. DNA Sequencing by: Washington
University Genome Sequencing Center St. Louis.
Putative full length read
The vector to vector length is 68.
Location/Qualifiers
1..67
/organism="Heterodera glycines"
/mol_type="mRNA"
/db_xref="taxon:51029"
/dev_stage="enriched for 2nd stage juveniles"
/lab_host="DH10B"
/clone_id="Heterodera glycines J2 PAMPI v8 Chiapelli
McCarter"
/note="Vector: PAMPI (Gibco); Site 1: NotI; Site 2: SalI;
The library was constructed by Brandi Chiapelli and Dr.
James McCarter at Washington University, St. Louis. The
cDNA was made by using Dynabead oligo-dT priming (Dynal).
PCR based library using a modified protocol from the SMART
PCR cDNA Synthesis Kit from Clontech. Directionally cloned
into the UDG sites of PAMPI. Nematodes are the OP25
strain. Frozen J2 nematodes were provided by Dr. Rick
Davis of North Carolina State University"

ORIGIN

ORIGIN

/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
/clone="MHP302k23"
/clone_lib="MHP"

Query Match 68.0%; Score 13.6; DB 11; Length 77;
Best Local Similarity 80.0%; Pred. No. 1e+05;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 ATAAAGCTTCTTCAAC 20
|||||
10 ATAAAGTTACATCTAC 29

RESULT 25
BM094204/c 78 bp mRNA linear EST 16-JUN-2004
bah26f06.y1 Gm-c1036 glycine max cDNA clone GENOME SYSTEMS CLONE
ID: Gm-c1036-2579 5', mRNA sequence.
ACCESSION BM094204 GI:17023170
VERSION EST.
KEYWORDS Glycine max (soybean)
SOURCE Glycine max
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
1 (bases 1 to 78)
Shoemaker,R., Kaim,P., Vodkin,L., Erpelting,J., Coryell,V., Khanna,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Pearson,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.
Public Soybean EST Project
Unpublished (1999)
Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
When it has been determined, an EST from the other end of this clone is listed in the 'Other ESTs on clone' field. Putative full length read vector to vector length is 79 this clone is available through: Biogenetic Services, 801 32nd Ave. Brookings, SD 57006 USA (phone: 605 423 4163; email: info@biogeneticservices.com).
Location/Qualifiers

FEATURES

source

1..78
/organism="Glycine max"
/mol_type="mRNA"
/cultivar="Jack"
/db_xref="taxon:3847"
/clone="GENOME SYSTEMS CLONE ID: Gm-c1036-2579"
/tissue_type="seomatic embryos cultured on MSD 20"
/lab_host="DH10B"
/clone_lib="Gm-c1036"
/note="Vector: pSPORT1; Site 1: NotI; Site 2: SalI; This cDNA library was constructed from mRNA isolated from somatic embryos (age ranging from 2 months to 9 months) cultured on MSD 20. The library was prepared using the Life Technologies pSuperScript cDNA library construction kit. Complementary DNA was synthesized from mRNA using a poly (dT) sequence with a NotI restriction site. SalI linkers adapters were ligated to the blunt-ended cDNA fragments followed by NotI digestion. The cDNA fragments were directionally cloned into the NotI-SalI restriction site of the pSPORT1 vector. The ligated cDNA fragments were transformed into E.coli Electromax DH10B host cells.

ORIGIN

This library was constructed in the laboratory of Dr. Lila Vodkin by Ann Khanna at the University of Illinois at Urbana-Champaign. e-mail: l-vodkin@uiuc.edu

Query Match 68.0%; Score 13.6; DB 3; Length 78;
Best Local Similarity 80.0%; Pred. No. 1e+05;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 ATAAAGCTTCTTCAAC 20
|||||
36 ATAAAGTTACATCTAC 17

RESULT 26
BF718349/c 59 bp mRNA linear EST 02-JAN-2001
EST122 microdissected normal human epidermis Homo sapiens cDNA
clone S81230.NIH-39 3', mRNA sequence.
ACCESSION BF718349 GI:12017448
VERSION EST.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 59)
Darling,T.N., Koh,B.B and Yancey,K.B.
Delineation of Genes Expressed in Human Epidermis by Large-Scale Sequencing of a cDNA Library from Laser Capture Microdissected Skin U. Invest. Dermatol. 112 (4), 673 (1999)
Contact: Yancey, K.B.
Dermatology Branch
National Cancer Institute
Building 10, Room 12N238, 10 Center Drive MSC 1908, Bethesda, MD 20892-1908, USA
Tel: 301 402 1863
Fax: 301 496 5370
Seq primer: M13R
High quality sequence stop: 59.
Location/Qualifiers

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

FEATURES

source

1..59
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="S81230.NIH-39"
/sex="Male"
/tissue_type="epidermis"
/dev_stage="adult"
/clone_lib="microdissected normal human epidermis"
/note="Organ: skin; Vector: pAP1; Epidermis from 20 cryostat skin sections (8 um thick) was selectively isolated using laser capture microdissection. Total RNA was extracted, reverse transcribed, and directionally cloned using uracyl DNA glycosylase (Kriizman protocol 2, see http://www.ncbi.nlm.nih.gov/GAP/info/libconst.cgi#Protocol2)."
CGAP/info/libconst.cgi#Protocol2)."

ORIGIN

Query Match 67.0%; Score 13.4; DB 2; Length 59;
Best Local Similarity 93.3%; Pred. No. 1.2e+05;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TAAAGCTTCTTCA 16
|||||
16 TAAAGCTTCTTCA 2

RESULT 27
CN855909/c 64 bp mRNA linear EST 03-JUN-2004
LOCUS CN855909
DEFINITION 000721AAAM003533HT (AAAA) Royal Gala 59 DAFB fruit, seeds removed

source

1.54
/organism="Glossina morsitans morsitans"
/mol_type="mRNA"
/sub_species="morsitans"
/db_xref="taxon:37546"
/clone="Tse119g02.q1c"
/tissue_type="adult infected gut"
/clone_lib="Glossina morsitans morsitans adult infected gut"
/note="country: Zimbabwe; EST from adult gut infected with T.brucei"

ORIGIN

Query Match 68.0%; Score 13.6; DB 5; Length 54;
Best Local Similarity 80.0%; Pred. No. 9.7e+04;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 ATMAAAGCTTCTTCAACAC 20
18 ATATAAATCTTCTTGAACTC 37

Db

RESULT 22
BH865173 68 bp DNA linear GSS 05-AUG-2002
DEFINITION SALK_097512 Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK_097512, genomic survey sequence.
BH865173
BH865173.1 GI:22101071
GSS.
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eustosids II; Brassicales; Brassicaceae; Arabidopsids.
1 (bases 1 to 68)
Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shim,P., Zimmerman,J., and Ecker,J.R.
A Sequence-indexed library of insertion Mutations in the Arabidopsis Genome
Unpublished (2001)
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of TDNA.
Class: TDNA tagged.

FEATURES
source
Location/Qualifiers
1..68
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/ecotype="Col-0"
/db_xref="taxon:3702"
/clone="SALK_097512"
/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"

ORIGIN

Query Match 68.0%; Score 13.6; DB 9; Length 68;
Best Local Similarity 80.0%; Pred. No. 1e+05;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 ATMAAAGCTTCTTCAACAC 20

Db

23 AGAGAAAGCTTCTTCACTC 42

RESULT 23
AV560198 76 bp mRNA linear EST 23-FEB-2004
DEFINITION AV560198 Arabidopsis thaliana green siliques Columbia Arabidopsis thaliana cDNA clone SQ13h07F 3', mRNA sequence.
AV560198
AV560198.1 GI:8731624
EST.
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eustosids II; Brassicales; Brassicaceae; Arabidopsids.
1 (bases 1 to 76)
Asamizu,B., Nakamura,Y., Sato,S., and Tabata,S.
A large scale analysis of cDNA in Arabidopsis thaliana: Generation of 12,028 non-redundant expressed sequence tags from normalized and size-selected cDNA libraries
DNA Res. 7 (3), 175-180 (2000)
10907847
Contact: Erika Asamizu
The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL: <http://www.kazusa.or.jp/en/plant/>.

FEATURES
source
Location/Qualifiers
1..76
/organism="Arabidopsis thaliana"
/mol_type="mRNA"
/ecotype="Columbia"
/db_xref="taxon:3702"
/clone="SQ13h07F"
/tissue_type="green siliques"
/clone_lib="Arabidopsis thaliana green siliques Columbia"
/note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2: XhoI"

ORIGIN

Query Match 68.0%; Score 13.6; DB 1; Length 76;
Best Local Similarity 80.0%; Pred. No. 1e+05;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 ATMAAAGCTTCTTCAACAC 20
39 ACAAAACCATCTTGAACAC 58

Db

RESULT 24
CR103372 77 bp DNA linear GSS 05-JUL-2004
DEFINITION CR103372 Reverse strand read from insert in 3'HPT insertion targeting and chromosome engineering clone MHP102K23, genomic survey sequence.
CR103372.1 GI:49850772
GSS; genome survey sequence; MICEP.
MUS musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Murinae; Mus.
1 (bases 1 to 77)
Adams,D.J., Biggs,P.J., Cox,A.V., Davies,R.M., van der Weyden,L., Jonkers,J., Smith,J., Plumb,R.W., Taylor,R.G., Nishijima,I., Yu,Y., Rogers,J., and Bradley,A.
Direct Submission
Submitted (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. <http://www.sanger.ac.uk/MICEP>
Location/Qualifiers
1..77

FEATURES
source

ORIGIN

/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="U962M0047F07"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_1lb="Mouse 10kb plasmid U962M library"
/note="Vector: pMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g1473214|gb|AF129072.1), a copy-number inducible derivative of plasmid pL. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match

Best Local Similarity 68.0%; Score 13.6; DB 9; Length 49;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 1 ATAAAGCTTCTTCAACAC 20

Db 28 ATAGAACCTTATGCAACAC 9

RESULT 20

DN252834/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

DN252834 52 bp mRNA linear EST 30-JUN-2005
ACB-5ab7116.g1 Hydra UCE6- barcoded EST's Hydra magnipapillata
cDNA 5', mRNA sequence.
DN252834
DN252834.2 GI:68378215
EST.
Hydra magnipapillata
Hydra magnipapillata
Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroids; Anthomedusae;
Hydridae; Hydra.
1 (bases 1 to 52)
Bode, H., Blumberg, B., Steele, R., Wigge, P., Gee, L., Nguyen, Q.,
Martinez, D., Kibler, D., Hampton, S., Clifton, S., Page, D., Marras, M.,
Hillier, L., Martin, J., Wylie, T., Dante, M., Theising, B., Bowers, Y.,
Gibbons, M., Ritter, E., Bennett, J., Ronko, J., Tsagarelis, R.,
Maguire, L., Kennedy, S., Waterston, R. and Wilson, R.
Washu Hydra EST Project
Unpublished (2002)
On Mar 1, 2005 this sequence version replaced gi:60415302.
Contact: Hans Bode
Washu Hydra EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: estewartson.wustl.edu
Library material provided by Hans Bode & Dirk Lindgens, Univ. of
Calif., Irvine Library constructed by Dirk Lindgens, Univ. of
Calif., Irvine Library sequenced by Washington University Genome
Sequencing Center For information on obtaining a clone please
contact: Hans Bode (hnbode@uci.edu)
This trace has been recalled with phred
original value before phred recall for SL was 104
original value before phred recall for SR was 392
Seq primer: -40RP from Gibco.

FEATURES

source

ORIGIN

Query Match 68.0%; Score 13.6; DB 8; Length 52;
Best Local Similarity 80.0%; Pred. No. 9.6e+04;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 1 ATAAAGCTTCTTCAACAC 20

Db 50 AGAAATCTTCTTCAAC 31

RESULT 21

BX551631

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

COMMENT

BX551631 54 bp mRNA linear EST 10-OCT-2003
BX551631 Glossina morsitans morsitans adult infected gut Glossina
morsitans morsitans cDNA clone Tse119g02_g1c, mRNA sequence.
BX551631
BX551631.1 GI:33375953
EST.
Glossina morsitans morsitans
Glossina morsitans morsitans
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Hippoboscidae; Glossinidae; Glossina.
1 (bases 1 to 54)
Lehane, M.J., Akroy, S., Gibson, W., Kerhornou, A., Berriman, M.,
Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N.
Adult midgut expressed sequence tags from the tsetse fly Glossina
morsitans morsitans and expression analysis of putative immune
response genes
Genome Biol. 4 (10), R63 (2003)
14519198
Contact: Hall N
Pathogen Sequencing Unit
The Sanger Institute The Wellcome Trust Genome Campus
Hinxton, Cambridge, CB10 1SA, UK
Request for clones, please contact: Mike Lehane
Prof. M.J. Lehane
School of Biological Sciences,
University of Wales,
Bangor LL57 2UW
All clones with suffix g1c are reverse primer reads starting at 5'
end of the cDNA all plc reads are from
the 3' end.
Location/Qualifiers

using P and piggyBac
Nat. Genet. 36 (3), 283-287 (2004)
PUBMED
14981521
COMMENT
Contact: Roger A Hoskins

FEATURES
source

Query Match	68.0%	Score 13.6	DB 10	Length 40
Best Local Similarity	80.0%	Pred. No. 9.1e+04		
Matches 16	Conservative	0	Mismatches 4	Indels 0
				Gaps 0

RESULT 18	42 bp	mRNA	linear	EST 28-JUL-2004
CA964102/c				
LOCUS	CA964102			
DEFINITION	CCIL02a07015f1	Carp liver	library 2	Cyprinus carpio. cDNA clone
	07015, mRNA	sequence.		

REFERENCE	AUTHORS	TITLE	JOURNAL	PUBLISHED	COMMENT
1	(bases 1 to 42)				
	Gracey, A.Y., Fraser, E.J., Li, W., Fang, Y., Taylor, R.R., Rogers, J., Brass, A., and Cossins, A.R.	Coping with cold: An integrative, multi-tissue analysis of the transcriptome of a poikilothermic vertebrate	Proc. Natl. Acad. Sci. U.S.A.	101 (48), 16970-16975 (2004)	
	155050548				
	On Jan 3, 2003 this sequence version replaced gi:27490659.				

FEATURES
source 1. .42
 Street, Liverpool, United Kingdom, L69 7ZB
 Tel: +44(0)151-795-4510
 Fax: +44(0)151-795-4431
 Email: cosins@liv.ac.uk
 Vector has been trimmed from this EST.
 plate: 07 row: 0 column: 15
 Seq primer: triplex 5' LD (5'-CTCGGAGCGGCCATTGTGTGGT-3')
 High quality sequence stop: 42
 POLYA=No.
 Location/qualifiers
 1. .42

ORIGIN

Query Match	68.0%	Score 13.6	DB 6	Length 42
Best Local Similarity	80.0%	Pred. 13.9	2e+04	
Matches 16	Conservative	0	Mismatches 4	Indels 0
				Gaps 0

RESULT 19	LOCUS	DEFINITION
AZ794039/c	AZ794039	49 bp DNA linear GSS 16-FEB-2001
	2M0047F07R	Mouse 10kb plasmid U06C1M library Mus musculus genomic clone U06C2M0047F07 R, genomic survey sequence.

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1 (Pages 1 to 49)	Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Rilly, M., Rose, M., Stokas, R., Tingey, A., von Niederhausen, A. and Wright, D., Weiss, R.	Mouse whole genome scaffolding with paired end reads from 10kb		
		plasmid inserts		
		Unpublished (2000)		
	Contact: Robert B. Weiss			

FEATURES	Location/Qualifiers
source	1. .49
	/organism="Mus musculus"
	/mol_type="genomic DNA"

```

RESULT 15
T74169/c
LOCUS
DEFINITION
774169
80 bp mRNA linear EST 02-MAR-1995
Y60612.81 Stratiogene liver (#937224) Homo sapiens cDNA clone
IMAGE:85054.3' similar to gb:U06977 SEBUM ALBUMIN PRECURSOR
(HUMAN)'', mRNA sequence.

ACCESSION
T74169
VERSION
T74169.1 GI:690844
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
REFERENCE
1 (bases 1 to 80)
Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiappelli,B.,
Chisoe,S., Dietrich,N., Dubuque,T., Favello,A., Gibb,W.,
Hawkins,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N.,
Mardis,E., Moore,B., Morris,M., Parsons,J., Prange,C., Rifkin,L.,
Rohlfing,T., Schellenberg,K., Soares,M.B., Tan,F., Thierry-Mieg,J.,
Trevisan,E., Underwood,K., Wohlmann,P., Waterston,R., Wilson,R.
and Warrir,M.
Generation and analysis of 280,000 human expressed sequence tags
Genome Res. 6 (9), 807-828 (1996)
JOURNAL
PUBMED
8889549
COMMENT
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
Insert Size: 58
High quality sequence starts: 1 High quality sequence stops: 1
Source: IMAGE Consortium, LIND. This clone is available royalty-free
through LIND; contact the IMAGE Consortium (info@image.lind.gov)
for further information. Trace considered overall poor quality
Insert Length: 58 Std Error: 0.00
Seq primer: -21m13
High quality sequence stop: 1.
FEATURES
source
1..80
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:502111"
/db_xref="taxon:9606"
/clone="IMAGE:85054"
/sex="male"
/dev_stage="49 years old"
/lab_host="SOLR cells (kanamycin resistant)"
/clone_lib="Stratiogene liver (#937224)"
/note="Organ: liver; Vector: pBlueScript SK; Site 1:
EcoRI; Site 2: XhoI; Cloned unidirectionally. Primer:
Oligo dT; Hepatectomy from normal male caucasian. Average
insert size: 1.1 kb; Uni-ZAP XR Vector; ~5' adaptor
sequence: 5' GAATTCGGCAGCAG 3' ~3' adaptor sequence: 5'
CTCGAGTTTCTTTTCTTTTCTTTT 3'"
ORIGIN
Query Match 69.0%; Score 13.8; DB 8; Length 80;
Best Local Similarity 88.2%; Pred. No. 8.5e+04;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Cy 2 TAAAGCTTCTTCAAC 18
Db 28 TAAAGCTTATTCATC 12
RESULT 16
BX558717/c
LOCUS
DEFINITION
BX558717 Glosina morsitans morsitans adult infected gut Glosina
morsitans morsitans cDNA clone Tse3d01_q1c, mRNA sequence.
ACCESSION
BX558717

```

```

VERSION
BX558717.1 GI:33365662
KEYWORDS
EST.
SOURCE
Glosina morsitans morsitans
ORGANISM
Glosina morsitans morsitans
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Hippoderoidea; Glosinidae; Glosina.
REFERENCE
1 (bases 1 to 38)
Lehane,M.J., Aksoy,S., Gibson,W., Keshornou,A., Berriman,M.,
Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
Adult midgut expressed sequence tags from the tsetse fly Glosina
morsitans morsitans and expression analysis of putative immune
response genes
Genome Biol. 4 (10), R63 (2003)
JOURNAL
PUBMED
14519198
COMMENT
Contact: Hall N
Pathogen Sequencing Unit
The Sanger Institute The Wellcome Trust Genome Campus
Hinxton, Cambridge, CB10 1SA, UK
Request for clones, please contact: Mike Lehane
Prof. M.J.Lehane
School of Biological Sciences,
University of Wales,
Bangor LL57 2UW
All clones with suffix q1c are reverse primer reads starting at 5'
end of the cDNA all p1c reads are from
the 3' end.
FEATURES
source
1..38
Location/Qualifiers
/organism="Glosina morsitans morsitans"
/mol_type="mRNA"
/sub_species="morsitans"
/db_xref="taxon:37546"
/clone="Tse3d01_q1c"
/tissue_type="adult infected gut"
/clone_lib="Glosina morsitans morsitans adult infected
gut"
/note="country: Zimbabwe; EST from adult gut infected with
T.Druce1"
ORIGIN
Query Match 68.0%; Score 13.6; DB 5; Length 38;
Best Local Similarity 80.0%; Pred. No. 9e+04;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Cy 1 ATAAAGCTTCTTCAACAC 20
Db 24 ATTAATAATTGTTCACAC 5
RESULT 17
C2487745
LOCUS
DEFINITION
C2487745 40 bp DNA linear GSS 29-APR-2005
f05125-5prime Exelixis piggyBac WH insertions Drosophila
melanogaster genomic Sequence recovered from 5' end of piggyBac,
genomic survey sequence.
ACCESSION
C2487745
VERSION
C2487745.1 GI:62985183
KEYWORDS
GSS.
SOURCE
Drosophila melanogaster (fruit fly)
ORGANISM
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
REFERENCE
1 (bases 1 to 40)
Thibault,S.T., Singer,M.A., Miyazaki,W.Y., Milash,B., Dompe,N.A.,
Singh,C.M., Buchholz,R., Demsky,M., Fawcett,R., Francis-Iang,H.L.,
Ryner,L., Cheung,L.M., Chong,A., Erickson,C., Fisher,W.W.,
Greer,K., Hartouni,S.R., Howie,E., Jakubila,B., Joo,D., Kilpack,K.,
Laufer,A., Mazzotta,J., Smith,R.D., Stevens,L.M., Stuber,C.,
Tan,L.R., Ventura,R., Woo,A., Zakrzenski,I., Zhao,L., Chen,F.,
Swimmer,C., Kocyanski,C., Duyk,G., Winberg,M.L. and Margolis,J.
A complementary transposon tool kit for Drosophila melanogaster

```

/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/db_xref="taxon:3702"
/clone_id="409A08"
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
/ecotype="Maassliewijkja"
1..58
/note="T-DNA flanking sequence
left border"

ORIGIN

Query Match 69.0%; Score 13.8; DB 10; Length 58;
Best Local Similarity 88.2%; Pred. No. 7.9e+04;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ATAAAGCTCTTCAA 17
30 AAAAAAGCTCTTTAA 14

RESULT 13
CG511973 65 bp mRNA linear GSS 01-OCT-2003
LOCUS OST64653 Mus musculus 129Sv/Ev Mus musculus CDNA clone OST64653,
DEFINITION mRNA sequence.
ACCESSION CG511973
VERSION CG511973.1 GI:37297765
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.

REFERENCE

AUTHORS

Zambrowicz,B.P., Abuin,A., Ramirez-Solis,R., Richter,L.J.,
Piggott,J., BeltrandelRio,H., Buxton,B.C., Edwards,J., Finch,R.A.,
Fridde,C.J., Gupta,A., Hansen,G., Hu,Y., Huang,W., Jang,C.,
Key,B.W., Jr., Kipp,P., Kohlhauff,B., Ma,Z.-Q., Markesch,D.,
Payne,R., Potter,D.G., Qian,N., Shaw,J., Schick,J., Shi,Z.-Z.,
Sparks,M.J., Van Sligtenhorst,I., Vogel,P., Walke,W., Xu,N.,
Zhu,Q., Person,C. and Sands,A.T.
Mnk1 kinase deficiency lowers blood pressure in mice: a gene-trap
screen to identify potential targets for therapeutic intervention
Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)
14610273
Contact: Zambrowicz BP
OmniBank

JOURNAL

PUBMED

COMMENT

Lexicon Genetics Incorporated
4000 Research Forest Drive, The Woodlands, TX 77381, USA
Email: materials@lexgen.com
Gene trap sequence tag generated by 3' RACE from mouse ES cells as
described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)
Class: Gene Trap.

FEATURES

Location/Qualifiers

1..65
/organism="Mus musculus"
/mol_type="mRNA"
/strain="129Sv/Ev"
/db_xref="taxon:10090"
/clone_id="OST64653"
/cell_type="embryonic stem cell"
/clone_lib="Mus musculus 129Sv/Ev"

ORIGIN

Query Match 69.0%; Score 13.8; DB 10; Length 65;
Best Local Similarity 78.9%; Pred. No. 8.1e+04;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 ATAAAGCTCTTCAA 19
46 AAAAAAGCTCTTCAA 64

RESULT 14
CR358067 65 bp DNA linear GSS 05-APR-2004
LOCUS Arabidopsis thaliana T-DNA flanking sequence GK-724C11-025362,
DEFINITION genomic survey sequence.
ACCESSION CR358067
VERSION CR358067.1 GI:45540989
KEYWORDS GSS.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1
Li,Y., Rosso,M.G., Strizhov,N., Viehoveer,P. and Weishaar,B.
GABI-Kat SimpleSearch: a flanking sequence tag (FST) database for
the identification of T-DNA insertion mutants in Arabidopsis
thaliana
Bioinformatics 19 (11), 1441-1442 (2003)
12874060

JOURNAL

PUBMED

AUTHORS

Rosso,M.G., Li,Y., Strizhov,N., Reiss,B., Dekker,K. and
Weishaar,B.
An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for
flanking sequence tag-based reverse genetics
Plant Mol. Biol. 53 (1-2), 247-259 (2003)
14756321

REFERENCE

AUTHORS

Strizhov,N., Li,Y., Rosso,M.G., Viehoveer,P., Dekker,K.A. and
Weishaar,B.
High-throughput generation of sequence indexes from T-DNA
mutagenized Arabidopsis thaliana lines
Biotechniques 35 (6), 1164-1168 (2003)
14682050

JOURNAL

PUBMED

AUTHORS

4 (bases 1 to 65)
Strizhov,N., Li,Y., Rosso,M.G. and Weishaar,B.
Direct SubMISSION
Submitted (31-MAR-2004) Weishaar B., Max-Planck-Institut fuer
Zuechtungsforchung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
This sequence has been recovered from the left border of the T-DNA.
It indicates an insertion close to or within gene At3g12400.
Details on the protocols used for generation of the sequence are
described in References 1-3. The sequences are generated at the MPI
for Plant Breeding Research in the context of the GABI-Kat project.
GABI-Kat is part of the German Plant Genomics program designated
'GABI'. Information on line availability can be found at:
<http://www.mpiz-koeln.mpg.de/GABI-Kat/>.

COMMENT

FEATURES

source

Location/Qualifiers
1..65
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/db_xref="taxon:3702"
/clone_id="GK-724C11-025362"
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
/ecotype="Col-0"
/note="PCR was performed on DNA from Arabidopsis thaliana
plants (Ti) which were transformed with the T-DNA from
vector pGAB1 (GenBank accession number: AY529716). The
lines contain one or more T-DNA insertions. The DNA
fragment (8) resulting from the PCR were directly sequenced
to determine the genomic sequence flanking the insertion.
T-DNA derived sequences were removed."

ORIGIN

Query Match 69.0%; Score 13.8; DB 11; Length 65;
Best Local Similarity 88.2%; Pred. No. 8.1e+04;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ATAAAGCTCTTCAA 17
Db 29 ATAAATACATCTTCAA 45

University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0178 row: A column: 15
 Seq primer: CGTTGTAAACGACGCCACGT
 Class: plasmid ends
 High quality sequence stop: 39.

FEATURES

SOURCE

1..39
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="U081M0178A15"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid U081M library"
 /note="Vector: PMD42HV; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 69.0%; Score 13.8; DB 9; Length 39;
 Best Local Similarity 88.2%; Pred. No. 7.3e+04;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 AAAAAGCTTCTCAACA 19
 ||| ||||| |||||
 Db 23 AAATGCTTCTTAACA 39

RESULT 11

LOCUS CD013073 56 bp mRNA linear EST 02-MAY-2003
 DEFINITION VWC054A09.395755 An expressed sequence tag database for abiotic stressed berries of *Vitis vinifera* var. Chardonnay
 CDNA clone VWC054A09.3, mRNA sequence.
 CD013073
 ACCESSION CD013073.1 GI:30329811
 KEYWORDS EST.
 SOURCE *Vitis vinifera*
 ORGANISM *Vitis vinifera*
 Eukaryota; Viridiplantae; Streptophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; Vitaceae; Vitis.

1 (bases 1 to 56)
 Cushman,J.C.

REFERENCE

An expressed sequence tag database for abiotic stressed berries of *Vitis vinifera* var. Chardonnay
 Unpublished (2002)

JOURNAL

Contact: Cushman JC
 Department of Biochemistry

University of Nevada
 MS200, Reno, NV 89557-0014, USA
 Tel: 775-784-1918
 Fax: 775-784-1650
 Email: jcushman@unr.edu
 PCR Primers
 FORWARD: T3 20mer
 BACKWARD: T7 21mer (backward)
 Plate: 054 row: A column: 09
 Seq primer: T22V (V=A,C,G)
 High quality sequence stop: 56.

FEATURES

SOURCE

1..56
 /organism="Vitis vinifera"
 /mol_type="mRNA"
 /db_xref="taxon:29760"
 /clone="VWC054A09"
 /issue_type="berries"
 /dev_stage="mixed: 8, 9, 11, 13, 15, 16 weeks daf"
 /clone_lib="An expressed sequence tag database for abiotic stressed berries of *Vitis vinifera* var. Chardonnay"
 /note="Vector: Lambda Uni-Zap XR, Bluescript SK-; Site_1: EcoRI; Site_2: XhoI"

ORIGIN

Query Match 69.0%; Score 13.8; DB 6; Length 56;
 Best Local Similarity 88.2%; Pred. No. 7.8e+04;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATAAAGCTTCTCAAC 17
 ||| ||||| |||||
 Db 37 ATGAAGCTTCTTAAC 53

RESULT 12

LOCUS AJ594977/c 58 bp DNA linear GSS 15-JAN-2004
 DEFINITION Arabidopsis thaliana T-DNA flanking sequence, left border, clone 409A08, genomic survey sequence.
 AJ594977
 ACCESSION AJ594977.1 GI:37944601
 VERSION GSS; left border; T-DNA flanking sequence.
 KEYWORDS Arabidopsis thaliana (thale cress)
 SOURCE Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE

1
 Brunaud V., Balzergue S., Dubreucq B., Aubourg S., Samson F., Chauvin S., Bechtold N., Cruaud C., Dekose R., Pelletier G., Lepoint J., Caboche M. and Lecharny A.
 T-DNA integration into the Arabidopsis genome depends on sequences of pre-insertion sites
 EMBO Rep. 3 (12), 1152-1157 (2002)

JOURNAL

2 (bases 1 to 58)
 Balzergue S.
 Direct Submission
 Submitted (23-OCT-2003) Balzergue S., UMRGV, INRA/CNRS, 2 rue Gaston Cremieux, 91057 Evry cedex, FRANCE

REFERENCE

PCR was performed on DNA from transformants of Arabidopsis thaliana plants from INRA (Versailles). The DNA fragment(s) resulting from the PCR were directly sequenced from the left or the right border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at <http://dbsgap.versailles.inra.fr/publications/>. This sequence has been generated in the framework of the French plant genomics program 'Genoplante' (<http://www.genoplante.com> and <http://genoplante-info.infobiogen.fr>).

FEATURES

SOURCE

1..58
 Location/Qualifiers

RESULT 8
BJ063523
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

BJ063523 32 bp mRNA linear EST 29-SEP-2003
BJ063523 NIBB Mochil normalized Xenopus tailbud library Xenopus
laevis cDNA clone XL076120 5', mRNA sequence.
BJ063523
BJ063523.1 GI:17424814
EST.
Xenopus laevis (African clawed frog)
Xenopus laevis
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
Xenopodinae; Xenopus; Xenopus.
1 (bases 1 to 32)
Kiyama, A., Terasaka, C., Mochil, M., Ueno, N., Shin-i, T. and
Kohata, Y.
Expressed genes in X. laevis embryo
Unpublished (2001)
Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6836
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp
The information of this clone is available through the following
URL.
http://xenopus.nibb.ac.jp/
Location/Qualifiers
1. 32
/organism="Xenopus laevis"
/mol_type="mRNA"
/db_xref="taxon:8355"
/clone="XL076120"
/tissue_type="whole embryo"
/dev_stage="stage 25"
/clone_lib="NIBB Mochil normalized Xenopus tailbud
library"

ORIGIN
Query Match 69.0%; Score 13.8; DB 3; Length 32;
Best Local Similarity 83.3%; Pred. No. 7e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 AAAAGCTTCTGAACAC 20
Db 14 AAAATGCTTTCAACAC 31

RESULT 9
CZ468098
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE

CZ468098 37 bp DNA linear GSS 29-APR-2005
C02650-Sprime Exelixis piggyBac PB insertions Drosophila
melanogaster genomic Sequence recovered from 5' end of piggyBac,
genomic survey sequence.
CZ468098
CZ468098.1 GI:62962111
GSS.
Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 37)
Thibault, S.T., Singer, M.A., Miyazaki, W.Y., Milash, B., Dompe, N.A.,
Singh, C.M., Buchholz, R., Demsky, M., Fawcett, R., Francis-Lang, H.L.,
Ryner, L., Cheung, L.M., Chong, A., Erickson, C., Fisher, W.W.,
Greer, K., Hartouni, S.R., Howie, B., Jaktula, L., Joo, D., Kilpack, K.,
Laufer, A., Mazzotta, D., Smith, R.D., Stevens, J.M., Stuber, C.,
Tan, L.R., Ventura, R., Woo, A., Zakirjsek, I., Zhao, L., Chen, F.,
Swimmer, C., Kopczyński, C., Duyk, G., Winberg, M.L. and Margolis, J.
A complementary transposon tool kit for Drosophila melanogaster

JOURNAL
PUBMED
COMMENT

using P and piggyBac
Nat. Genet. 36 (3), 283-287 (2004)
14981521
Contact: Roger A Hoskins
Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory
Mailstop 64-121, One Cyclotron Road, Berkeley, CA 94720, USA
Tel: 510 486 4015
Fax: 510 486 6798
Email: RHOskins@lbl.gov
Sequence recovery method was inverse PCR.
Sequence orientation is forward strand relative to 5' end of
piggyBac element.
The piggyBac insertion position is 34 in the 37 bases. This
insertion position refers to the first base of the 4 base TTAA
target recognition sequence.
Class: transposon insertion site.
Location/Qualifiers
1. 37
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/strain="isogenic w- strain"
/db_xref="taxon:7227"
/clone_lib="Exelixis piggyBac PB insertions"
/note="Vector: piggyBac PB (GenBank accession number
AY15146); An isogenic w- Drosophila melanogaster strain
was generated by remobilization of transposable
elements. We remobilized the PB element using
Hsp70:piiggyBac transposase from a single ammiton
element on either the X or third chromosome. We induced
transposase expression by immersing bottles in a
circulating 37°C water bath for a daily (days 3-10 after
egg-laying) 1-h heat shock. We outcrossed the resulting
dysgenic males to an isogenic w- strain. New insertions
were identified on the basis of a change in eye color
(third chromosome ammiton) or the appearance of w+ male
progeny (X chromosome ammiton). All lines were mapped
to a chromosome by standard genetic methods, examined for
homozygous viability, and used for recovery of flanking
genomic sequence by inverse PCR."

ORIGIN
Query Match 69.0%; Score 13.8; DB 10; Length 37;
Best Local Similarity 88.2%; Pred. No. 7.2e+04;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATAAAAAGCTTCTTCAA 17
Db 21 ATAAAAAGCTTCTTAA 37

RESULT 10
AZ407584
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

AZ407584 39 bp DNA linear GSS 03-OCT-2000
1M0178A15F Mouse 10kb plasmid UGCGM library Mus musculus genomic
clone UGCGM0178A15 F, genomic survey sequence.
AZ407584
AZ407584.1 GI:10531513
GSS.
Mus musculus (house mouse)
Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.
1 (bases 1 to 39)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, B., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tinney, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss

Query Match 71.0%; Score 14.2; DB 10; Length 75;
 Best Local Similarity 84.2%; Pred. No. 5.4e+04;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 1 ATAAAAGCTTCTTCAACA 19
 54 ATAAAAGCTTATTGACCA 72

RESULT 6
 AZ628248 76 bp DNA linear GSS 13-DEC-2000
 LOCUS 1M0480D16 Mouse 10kb plasmid U06C1M library Mus musculus genomic
 DEFINITION clone U06C1M0480D16 F, genomic survey sequence.
 ACCESSION AZ628248
 VERSION AZ628248.1 GI:11750438
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 76)
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, B., Pedersen, T.,
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
 Niederhausen, A. and Wright, D., Weis, R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0480 row: D column: 16
 Seq primer: CGTTGTAAACGACGCGCAGT
 Class: plasmid ends
 High quality sequence stop: 76.
 Location/Qualifiers

FEATURES
 source 1..76
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="U06C1M0480D16"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid U06C1M library"
 /note="Vector: pMD42nv, Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/shares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pMD42 (gi|4732114|gb|AF19072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

4 ORIGIN

Query Match 71.0%; Score 14.2; DB 9; Length 76;
 Best Local Similarity 84.2%; Pred. No. 5.4e+04;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 1 ATAAAAGCTTCTTCAACA 19
 37 AAAGAAGCATCTTCAACA 55

RESULT 7
 CD395443 80 bp mRNA linear EST 01-JUN-2003
 LOCUS Gm_cK15462 Soybean induced by Salicylic Acid Glycine max cDNA 3',
 DEFINITION mRNA sequence.
 ACCESSION CD395443
 VERSION CD395443.1 GI:31310240
 KEYWORDS EST.
 SOURCE Glycine max (soybean)
 ORGANISM Glycine max
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Eukaryota; Viridiplantae; eudicotyledons; core eudicotyledons;
 Spermatophyta; Magnoliophyta; eucommidiales; Fabales; Phaseolales;
 rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
 Glycine.
 1 (bases 1 to 80)
 Tian, A.G., Wang, J., Cui, P., Han, Y.J., Xu, H., Cong, L.J., Huang, X.G.,
 Wang, X.L., Jiao, Y.Z., Wang, B.J., Wang, Y.J., Zhang, J.S. and
 Chen, S.Y.
 Characterization of soybean genomic features by analysis of its
 expressed sequence tags
 Theor. Appl. Genet. 108 (5), 903-913 (2004)
 14624337
 Contact: Chen S-Y
 Plant Biotechnology Laboratory
 Institute of Genetics and Developmental Biology, CAS, China
 Datun road, Beijing 100101, China
 Tel: 86-10-6486859
 Fax: 86-10-64873428
 Email: sychen@genetics.ac.cn
 Email: sychen@genetics.ac.cn
 Seq primer: T7 primer.
 Location/Qualifiers

FEATURES
 source 1..80
 /organism="Glycine max"
 /mol_type="mRNA"
 /culturvar="Kefeng 1"
 /db_xref="taxon:3847"
 /tissue_type="Seedlings"
 /dev_stage="two-week seedlings"
 /lab_host="XLI-Blue MRF strain"
 /clone_lib="Soybean induced by Salicylic Acid"
 /note="Vector: pBluescript SK+, Site_1: EcoR I, Site_2:
 Xho I; The cDNA library was constructed by He, C-Y from
 mRNA isolated from two-week seedlings (cultivar Kefeng 1)
 treated by spraying 2.0mM salicylic acid for 24, 36, 48
 and 72 h. Complementary DNA was synthesized from mRNA
 using a primer consisting of a poly(AT) sequence with a
 blunt restriction site. EcoRI adaptors were ligated to the
 blunt-ended cDNA fragments followed by XhoI digestion. The
 cDNA fragments were directionally cloned into the
 EcoRI-XhoI restriction site of the pBluescript vector. The
 ligated cDNA fragments were transformed into XLI-Blue MRF
 host cells (Stratagene)."

ORIGIN

Query Match 70.0%; Score 14; DB 6; Length 80;
 Best Local Similarity 100.0%; Pred. No. 6.8e+04;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 4 AAAAGCTTCTTCAA 17
 54 AAAAGCTTCTTCAA 67

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

FEATURES
SOURCE

1 (bases 1 to 54)
Staten,N.R.
Direct Submission (Staten,N.R.)
Unpublished (2005)
Contact: Nick Staten
Tel: 636 247 6855
Email: nicholas.r.staten@pfizer.com.

location/Qualifiers
1..54
 /organism="Canis familiaris"
 /mol_type="mRNA"
 /strain="beagle"
 /db_xref="taxon:9615"
 /clone="CIN1579719"
 /tissue_type="liver"
 /lab_host="DH10B"
 /clone_id="LIB3187"
 /note="Vector: pSPORT1; Site 1: SalI; Site 2: NotI;
normal, untreated canine liver"

ORIGIN

Query Match 71.0% ; Score 14.2; DB 8; Length 54;
Best Local Similarity 84.2%; Pred. No. 5e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

CY

1 ATAAAGACTTCTTCACA 19
||| ||||| ||||| |||||
54 ATGAAMGCACTTTAACA 36

LOCUS

T89907/c

DEFINITION

T89907 57 bp mRNA linear EST 20-MAR-1995
yeilb09.r1 Scratogene lung (#937210) Homo sapiens cDNA clone
IMAGE:117401 5' similar to gb:L11566 60S RIBOSOMAL PROTEIN L18
(HUMAN); mRNA sequence.

ACCESSION

T89907

VERSION

T89907.1

KEYWORDS

GI:718420

SOURCE

EST.

ORGANISM

Homo sapiens (human)

Homio sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 57)
Hillier,L., Lennon,G., Becker,M., Bernaldo,M.F., Chiapelli,B.,
Chisoe,S., Dietrich,N., Dubugue,T., Pavello,A., Gish,W.,
Hawkins,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N.,
Mardis,E., Moore,B., Morris,M., Parsons,J., Prange,C., Rifkin,L.,
Rohlfing,I., Scheinberg,K., Soares,M.B., Tan,F., Thillery-Weg,J.,
Trevaskis,E., Underwood,K., Wohlmann,P., Waterston,R., Wilson,R.
and Marra,M.

Generation and analysis of 280,000 human expressed sequence tags
Genome Res. 6 (9), 807-828 (1996)

8889549

CONTACT: Wilson RK
Washington University School of Medicine
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
High quality sequence starts: 1
High quality sequence stops: 1
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Seq primer: M13RP1
High quality sequence stop: 1.
Location/Qualifiers
1..57
 /organism="Homo sapiens"
 /mol_type="mRNA"

ORIGIN	Query Match	Best Local Similarity	Matches	71.0%; 84.2%; 16; Conservative	Score 14.2; Pred. No. 5.1e+04; 0; Mismatches	DB 8; 5; Indels	Length 57; 0; Gaps
RESULT 5 AJ600260	1 ATAAAGCTTCTCAACA 19		39 ATAAACACCTTCTCAACA 21				
LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM	AJ600260 Arabidopsis thaliana T-DNA flanking sequence, right border, clone 503D03, genomic survey sequence. AJ600260 AJ600260.1 GI:37949888 GSS; right border; T-DNA flanking sequence. Arabidopsis thaliana (thale cress) Arabidopsis thaliana Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.	75 bp DNA linear GSS 15-JAN-2004					
REFERENCE AUTHORS TITLE	Brunaud, V., Balzerque, S., Dubreucq, B., Aubourg, S., Samson, F., Chauvin, S., Bechtold, N., Craud, C., DeRose, R., Pelletier, G., Lepiniec, L., Caboche, M., and Leclercq, A. T-DNA integration into the Arabidopsis genome depends on sequences of pre-insertion sites EMBO Rep. 3 (12), 1152-1157 (2002)						
COMMENT	12446565 2 (bases 1 to 75) Balzerque, S. Direct Submission Submitted (23-OCT-2003) Balzerque S., UMRGV, INRA/CNRS, 2 rue Gaston Cremieux, 91057 Evry cedex, FRANCE PCR was performed on DNA from transformants of Arabidopsis thaliana plants from INRA (Versailles). The DNA fragment(s) resulting from the PCR were directly sequenced from the left or the right border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at http://dbsgip.versailles.inra.fr/publiclines/ . This sequence has been generated in the framework of the French plant genomics program 'Genoplante' (http://www.genoplante.com and http://genoplante-info.inbiohogen.fr). Location/Qualifiers						
FEATURES source	1..75 /organism="Arabidopsis thaliana" /mol_type="genomic DNA" /db_xref="taxon:3702" /clone="503D03" /clone_1lb="Arabidopsis thaliana T-DNA insertion lines" /ecotype="Wassilewskija" 1..75 /note="T-DNA flanking sequence right border"						
ORIGIN	1..75 /organism="Arabidopsis thaliana" /mol_type="genomic DNA" /db_xref="taxon:3702" /clone="503D03" /clone_1lb="Arabidopsis thaliana T-DNA insertion lines" /ecotype="Wassilewskija" 1..75 /note="T-DNA flanking sequence right border"						

	12.6	63.0	56	9	BH23717	1006114E1
96	12.6	63.0	57	6	CA330935	haa94h05.
97	12.6	63.0	57	6	CB27096	1Ru34D1.1
98	12.6	63.0	57	10	CZ551924	CB2_393
c 99	12.6	63.0	57	10	BX894115	Arabidop
c 100	12.6	63.0	57	10	BX894115	Arabidop

ALIGNMENTS

RESULT 1	LOCUS	DEFINITION
AU009985	72 bp	mRNA linear EST 31-JUL-1998
AU009985	Schizosaccharomyces pombe late log phase cDNA	
Schizosaccharomyces pombe cDNA clone spc00766, mRNA sequence.		

ACCESSION	AU009985	
VERSION	AU009985.1	GI:334665
KEYWORDS	EST.	
SOURCE	Schizosaccharomyces pombe	(fission yeast)
ORGANISM	Schizosaccharomyces pombe	

REFERENCE	AUTHORS	TITLE
1 (bases 1 to 72)	Moriwyo, M. and Mita, K.	Identification of expressed sequence tags of <i>Schizosaccharomyces</i>

JOURNAL
Unpublished (1998)
Contact: Mitsuoki Morimyo
COMMENT

FEATURES	Location/Qualifiers
source	1. .72

```

/organism="Schizosaccharomyces pombe"
/mol_type="mRNA"
/strain="972"
/db_xref="taxon:4896"
/clone="spc00766"
/sex="h minus"
/clone_lib="Schizosaccharomyces pombe late log phase cDNA"
/note="Vector: M13mp19; The cDNA library of Schizosaccharomyces pombe was prepared by cloning cDNA into the SmaI site of M13mp19 DNA and the direction of DNA sequences was not always from 5' to 3'. The cDNA data of Schizosaccharomyces pombe are available for searching on the World Wide Web. (URL, http://www.nits.go.jp)"

```

Query March	72.0%	Score 14.4	DB 1	length 72
Best Local Similarity	93.8%	Pred. No. 4.3e+04		
Matches 15	Conservative 0	Mismatches 1	Indels 0	Gaps 0

QY	1	ATAAAAGCTTCTTCA	16
Db	22	AAAAAAGCTTCTTCA	37

RESULT 2	AZ435382	LOCUS	DEFINITION
	AZ435382	47 bp	DNA linear GSS 03-OCT-2000
	1M0222D23r	Mouse 10kb	plasmid UUG1M library Mus musculus genomic
	1M0222D23 F,	genomic	survey sequence.
	clone UUG1M0222D23		

ACCESSION	A2435382	
VERSION	A2435382.1	GI:10559395
KEYWORDS	GSS	
SOURCE	Mus musculus	(house mouse)
ORGANISM	Mus musculus	

REFERENCE 1 (bases 1 to 47)

AUTHORS
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,

ISLAMI, H., LONGACRE, S., MAMMOTH, M., MEENEN, D., PEUTERSEN, L.,
REILLY, M., ROSE, M., ROSE, R., STOKES, R., TINGEY, A., VON
NIEDERHAUSEN, A. and WRIGHT, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kx

JOURNAL COMMENT
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center

University of Utah
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606
Fax: 801 585 7177

```
Email: ddumogenetics.utcn.edu
Insert length: 10000 Std Error: 0.000
plate: 0222 row: D column: 23
Seq primer: CGTGTAAACGACGCGCCAGT
Class: plasmid ends
High quality sequence stop: 47.
```

FEATURES	Location/Qualifiers
source	1. .47

```

/organism="mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGC1M0222D23"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (gil4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

```

Query Match	71.0%	Score 14.2	DB 9	Length 47
Best Local Similarity	84.2%	Pred. No. 4.9e+04		
Matches 16	Conservative 0	Mismatches 3	Indels 0	Gaps 0

QY	1	ATAAAAAGCTTCTCACA	13
Db	13	ATAAAATCTTTAAAAA	31

RESULT 3	54 bp	RNA	linear	EST 04-MAR-2005
DN336224/c				
LOCUS	DN336224			
DEFINITION	LIB3187-017-P1-K1-G5 LIB3187	Canis	familiaris	CDNA clone
	CLN1579719,	mrna	sequence.	

ACCESSION	DN336224
VERSION	DN336224.1
KEYWORDS	EST.
SOURCE	Canis familiaris (dog)
ORGANISM	Canis familiaris

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae; Canis.

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 1, 2006, 22:32:40 ; Search time 2938 Seconds

(without alignments)
318.496 Million cell updates/sec

Title: US-10-653-528-32

Perfect score: 20

Sequence: 1 ataaaagcttcctcaacac 20

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 512758

Minimum DB seq length: 0

Maximum DB seq length: 80

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

EST: *
1: gb_est1: *
2: gb_est2: *
3: gb_est3: *
4: gb_hic: *
5: gb_est4: *
6: gb_est5: *
7: gb_est6: *
8: gb_est7: *
9: gb_gss1: *
10: gb_gss2: *
11: gb_gss3: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	14.4	72.0	72	1	AU009985 AU009985
2	14.2	71.0	47	8	AZ435382 AZ435382
3	14.2	71.0	54	8	DN336224 LIB3187-0
4	14.2	71.0	57	8	T89907 T89907
5	14.2	71.0	75	10	AJ600260 AJ600260
6	14.2	71.0	76	9	AZ628248 AZ628248
7	14	70.0	80	6	CD395443 CD395443
8	13.8	69.0	32	3	BJ063523 BJ063523
9	13.8	69.0	37	10	CZ468098 CZ468098
10	13.8	69.0	39	9	AZ407584 AZ407584
11	13.8	69.0	56	6	CD013073 CD013073
12	13.8	69.0	58	10	AJ594977 AJ594977
13	13.8	69.0	65	10	CG511973 CG511973
14	13.8	69.0	65	11	CR358067 CR358067
15	13.8	69.0	80	8	T74169 T74169
16	13.6	68.0	38	5	BX558717 BX558717
17	13.6	68.0	40	10	CZ487745 CZ487745
18	13.6	68.0	42	6	CA964102 CA964102
19	13.6	68.0	49	9	AZ794039 AZ794039
20	13.6	68.0	52	8	DN252834 DN252834
21	13.6	68.0	54	5	BX551631 BX551631
22	13.6	68.0	68	9	BH865173 BH865173

23	13.6	68.0	76	1	AV560198 AV560198
24	13.6	68.0	77	11	CR103372 CR103372
25	13.6	68.0	78	3	BM094204 BM094204
26	13.4	67.0	59	2	BF718349 BF718349
27	13.4	67.0	64	7	CN855909 CN855909
28	13.4	67.0	65	10	AG222033 AG222033
29	13.4	67.0	67	3	BI749485 BI749485
30	13.4	67.0	68	10	CG613923 CG613923
31	13.4	67.0	73	10	BX945947 BX945947
32	13.4	67.0	74	6	CD409537 CD409537
33	13.4	67.0	78	1	AA128473 AA128473
34	13.2	66.0	40	1	AA615668 AA615668
35	13.2	66.0	42	9	CC888626 CC888626
36	13.2	66.0	49	10	CZ485190 CZ485190
37	13.2	66.0	51	6	CA340051 CA340051
38	13.2	66.0	55	8	D18199 D18199
39	13.2	66.0	57	1	AA515833 AA515833
40	13.2	66.0	62	9	AZ922433 AZ922433
41	13.2	66.0	66	9	BH904156 BH904156
42	13.2	66.0	66	10	CL308540 CL308540
43	13.2	66.0	67	6	CF269390 CF269390
44	13.2	66.0	67	9	AZ77832 AZ77832
45	13.2	66.0	67	10	AJ594453 AJ594453
46	13.2	66.0	68	6	CD906882 CD906882
47	13.2	66.0	68	7	CV582865 CV582865
48	13.2	66.0	68	10	CL521961 CL521961
49	13.2	66.0	69	6	CD906653 CD906653
50	13.2	66.0	70	1	AM692693 AM692693
51	13.2	66.0	70	6	CD906881 CD906881
52	13.2	66.0	70	10	CZ020820 CZ020820
53	13.2	66.0	71	3	BP083358 BP083358
54	13.2	66.0	72	1	AA222256 AA222256
55	13.2	66.0	73	6	CD614966 CD614966
56	13.2	66.0	75	1	A1540552 A1540552
57	13.2	66.0	75	5	BX718806 BX718806
58	13.2	66.0	76	1	AA123303 AA123303
59	13.2	66.0	76	1	AV854443 AV854443
60	13.2	66.0	76	6	CD614965 CD614965
61	13	65.0	26	10	CZ194604 CZ194604
62	13	65.0	27	10	CZ194654 CZ194654
63	13	65.0	27	6	CB176362 CB176362
64	13	65.0	72	3	BM570537 BM570537
65	13	65.0	76	3	BI900300 BI900300
66	12.8	64.0	53	9	AZ767745 AZ767745
67	12.8	64.0	55	1	AA512048 AA512048
68	12.8	64.0	57	9	BH805389 BH805389
69	12.8	64.0	59	9	CC455769 CC455769
70	12.8	64.0	62	10	CZ470358 CZ470358
71	12.8	64.0	64	7	BJ047871 BJ047871
72	12.8	64.0	64	7	CN949564 CN949564
73	12.8	64.0	65	10	CL423453 CL423453
74	12.8	64.0	69	6	CF327597 CF327597
75	12.8	64.0	70	6	CB165090 CB165090
76	12.8	64.0	71	8	T74760 T74760
77	12.8	64.0	75	1	AU012915 AU012915
78	12.8	64.0	75	7	CN867837 CN867837
79	12.8	64.0	76	8	D19177 D19177
80	12.8	64.0	77	8	T63760 T63760
81	12.8	64.0	78	3	BM445430 BM445430
82	12.8	64.0	78	10	CG559328 CG559328
83	12.6	63.0	31	9	AZ773758 AZ773758
84	12.6	63.0	33	9	BZ596399 BZ596399
85	12.6	63.0	37	11	TN11602P TN11602P
86	12.6	63.0	39	10	CZ471534 CZ471534
87	12.6	63.0	40	1	AU254534 AU254534
88	12.6	63.0	48	9	BH758136 BH758136
89	12.6	63.0	50	11	CR161437 CR161437
90	12.6	63.0	52	9	AZ694935 AZ694935
91	12.6	63.0	52	10	AJ942823 AJ942823
92	12.6	63.0	54	9	BH809975 BH809975
93	12.6	63.0	55	1	AJ239854 AJ239854
94	12.6	63.0	56	3	BI855869 BI855869
95	12.6	63.0	56	7	CR418823 CR418823

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ID AAT58883 standard; DNA; 45 BP.
 AC AAT58883;
 XX
 DT 28-OCT-1997 (first entry)
 XX
 DE Monospecific tetravalent antigen-binding peptide primer BGI.
 XX
 KM Multippecific; multivalent; ligand binding polypeptide; prophylactic;
 KM antigen binding site; hapten; enzyme; bivalent antibody; T cell;
 KM polymerase chain reaction; PCR; ss.
 XX
 OS Synthetic.
 XX
 PN WO9701580-A1.
 XX
 PD 16-JAN-1997.
 XX
 PF 26-JUN-1996; 96WO-US010905.
 XX
 PR 27-JUN-1995; 95US-00495209.
 XX
 PA (SCRI) SCRIPPS RES INST.
 XX
 PI Kang AS;
 XX
 DR WPI; 1997-100168/09.
 XX
 PT Multi-specific and multi-valent ligand binding polypeptide(s) - comprise
 PT one or more antigen binding sites, for use in diagnostic, prophylactic
 PT and therapeutic methods.
 XX
 PS Example 7; Page 90; 126pp; English.
 XX
 CC A novel composition has been produced which comprises a bivalent
 CC polypeptide having an amino acid residue sequence of formula: V - X - V
 CC where V = an antigen binding site; X = an amino acid residue sequence of
 CC 5 to 120 amino acid residues. The present sequence represents the PCR
 CC primer BGI used in the preparation of anti-CD3 monospecific tetravalent
 CC antigen-binding polypeptide. The polypeptides can assume a conformation
 CC having a binding site specific for a preselected or predetermined ligand
 CC such as an antigen, hapten or enzymatic substrate. They can be used in
 CC diagnostic assays and also for prophylactic or therapeutic applications.
 CC The bivalent antibodies can also be used for activating and crosslinking
 CC T cells in vitro or in vivo. The polypeptides exist in stable
 CC conformations and bind to target molecules with high avidity while
 CC lacking undesirable effector or complement activation functions, to
 CC provide functional molecules which can circulate in the body for longer
 CC periods of time than their Fab counterparts
 XX
 SQ Sequence 45 BP; 9 A; 18 C; 8 G; 10 T; 0 U; 0 Other;
 Query Match 72.0%; Score 14.4; DB 2; Length 45;
 Best Local Similarity 93.8%; Pred. No. 8.3e+03;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 4 AAAAGCTTCTCAACA 19
 Db 45 AAGAGCTTCTCAACA 30

Search completed: March 1, 2006, 22:51:44
 Job time : 341.667 secs

CC the transposon vector transposes into the DNA. The method is useful for
CC altering deoxyribonucleic acid (DNA) in *Sorangium* host cell, for example,
CC so that the cells produce useful molecules such as polyketides. The
CC current sequence represents a primer used in an example from the
CC invention in the cloning of the *C. carnea* mariner transposase gene.

XX Sequence 33 BP; 12 A; 8 C; 4 G; 9 T; 0 U; 0 Other;

Query Match 72.0%; Score 14.4; DB 12; Length 33;
Best Local Similarity 93.8%; Pred. No. 8.1e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 AAAAGCTTCTTCAACA 19
DB 1 AAAAGCTTATTCACACA 16

RESULT 28
AAD52829/c
ID AAD52829 standard; DNA; 42 BP.

XX AAD52829;

XX 14-MAY-2003 (first entry)

DE Human Mowgli G-protein coupled receptor DNA amplifying primer #2.

XX Mowgli G-protein coupled receptor; GPCR; immune response; infection;
XX neurological disorder; Parkinson's disease; obesity; asthma; cancer;
XX anorexia; pain; diabetes; vaccine; human; PCR; primer; ss.

XX Homo sapiens.

XX WO200292624-A2.

XX 21-NOV-2002.

XX 16-MAY-2002; 2002WO-GB002304.

XX 16-MAY-2001; 2001GB-00011959.

XX 18-MAY-2001; 2001US-0292141P.

XX (PARA-) PARADIGM THERAPEUTICS LTD.

XX Carlton M, Aparicio S, Dixon J, Thresher R, Zahn D;

XX WPI; 2003-129261/12.

XX New Mowgli G-protein coupled receptor polypeptides and polynucleotides,
XX useful for inducing immunological response to produce antibody and/or T
XX cell immune response against e.g. bacterial, fungal, protozoan or viral
XX infections.

XX Example 2; Page 92; 121pp; English.

XX The invention relates to novel Mowgli G-protein coupled receptor (GPCR)
XX polypeptides and polynucleotides. Mowgli polypeptides, nucleic acids,
XX probes, antibodies, expression vectors and ligands are useful as
XX biosensors, for detection, diagnosis, or treatment of diseases associated
XX with over-, under- or abnormal expression of Mowgli GPCR in tissues. In
XX genetic analysis and in chromosome identification. Polypeptides of the
XX invention may be used for screening compounds which bind the receptor and
XX which activate (agonists) or inhibit (antagonists) activation of Mowgli.
XX They may further be used as vaccines to induce immunological response to
XX produce antibody and/or T cell immune response against e.g. bacterial,
XX protozoan, fungal or viral infections, pain, cancers, diabetes, obesity,
XX anorexia, asthma, Parkinson's disease and other neurological disorders.
XX The present sequence is human Mowgli G-protein coupled receptor DNA
XX amplifying PCR primer used in the exemplification of the invention

XX Sequence 42 BP; 13 A; 5 C; 7 G; 17 T; 0 U; 0 Other;

Query Match 72.0%; Score 14.4; DB 8; Length 42;

Best Local Similarity 93.8%; Pred. No. 8.3e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATAAAAAGCTTCTTCA 16
DB 41 ATAAAAAGCTTCTTCA 26

RESULT 29
ABSS5373/c
ID ABSS5373 standard; DNA; 44 BP.

XX ABSS5373;

XX 16-DEC-2002 (first entry)

DE Arabidopsis thaliana DNA damage-responding promoter sequence.

XX Cis control sequence; DNA damage-responding gene expression;
XX DNA damage-responding promoter; plant expression cassette;
XX transformed plant cell; plant; ds.

XX Arabidopsis thaliana.

XX JP2002272469-A.

XX 24-SEP-2002.

XX 19-MAR-2001; 2001JP-00079524.

XX 19-MAR-2001; 2001JP-00079524.

XX (NARA-) NARA SENTAN KAGAKU GIJUTSU DAIGAKUIN DAI.

XX WPI; 2002-718706/78.

XX Cis control sequence showing a capacity of controlling DNA damage-
XX responding gene expression of a higher plant, a DNA damage-responding
XX promoter, an expression cassette for a plant.

XX Claim 1; Fig 5; 19pp; Japanese.

XX The present invention relates to a cis control sequence showing a
XX capacity for controlling DNA damage-responding gene expression of a
XX higher plant, a plant (Arabidopsis thaliana) DNA damage-responding
XX promoter, and an expression cassette for a plant. The invention describes
XX an expression cassette for a plant for expressing an exotic gene, by
XX responding to DNA damage containing the above promoter and a site for
XX inserting an exotic gene, so that said exotic gene is linked to said
XX promoter expressably. Also described is a recombinant plasmid for
XX expressing an exotic gene by responding to DNA damage containing the
XX above promoter and an exotic gene linked expressably to said promoter, a
XX method for acquiring a plant cell transformed by an exotic gene wherein a
XX specific expression responding to DNA damage is desired including a step
XX of transforming a plant cell with the above recombinant plasmid to get a
XX transformed plant cell, and a transformed plant cell prepared by the
XX above method. The method is used for acquiring a plant cell transformed
XX by an exotic gene. The present sequence represents Arabidopsis thaliana
XX DNA damage-responding promoter sequence

XX Sequence 44 BP; 10 A; 11 C; 10 G; 13 T; 0 U; 0 Other;

Query Match 72.0%; Score 14.4; DB 6; Length 44;
Best Local Similarity 93.8%; Pred. No. 8.3e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 AAAAGCTTCTTCAACA 19
DB 30 AAAAGCTTCTTCAACA 15

RESULT 30
AAT58883/c

PF 19-MAR-2001; 2001JP-00079524.
XX
PR 19-MAR-2001; 2001JP-00079524.
XX
PA (NARA-) NARA SENTAN KAGAKU GIJUTSU DAIGAKUIN DAT.
XX
DR WPI; 2002-718706/78.
XX
PT CIs control sequence showing a capacity of controlling DNA damage-
PT responding gene expression of a higher plant, a DNA damage-responder
PT promoter, an expression cassette for a plant.
XX
PS Example 4; Page 12; 19pp; Japanese.
XX
CC The present invention relates to a cis control sequence showing a
CC capacity for controlling DNA damage-responder gene expression of a
CC higher plant, a plant (Arabidopsis thaliana) DNA damage-responder
CC promoter, and an expression cassette for a plant. The invention describes
CC an expression cassette for a plant for expressing an exotic gene, by
CC responding to DNA damage containing the above promoter and a site for
CC inserting an exotic gene, so that said exotic gene is linked to said
CC promoter expressably. Also described is a recombinant plasmid for
CC expressing an exotic gene by responding to DNA damage containing the
CC above promoter and an exotic gene linked expressably to said promoter, a
CC method for acquiring a plant cell transformed by an exotic gene wherein a
CC specific expression responding to DNA damage is desired including a step
CC of transforming a plant cell with the above recombinant plasmid to get a
CC transformed plant cell, and a transformed plant cell prepared by the
CC above method. The method is used for acquiring a plant cell transformed
CC by an exotic gene. The present sequence represents a primer used in the
CC examples of the present invention
XX
SQ Sequence 29 BP; 9 A; 7 C; 5 G; 8 T; 0 U; 0 Other;
XX
Query Match 72.0%; Score 14.4; DB 6; Length 29;
Best Local Similarity 93.8%; Pred. No. 8e+03; 1; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 4 AAAAGCTTCTTCAACA 19
Db 7 AAAGCTTCTTCAACA 22
XX
RESULT 26
ABSS5383/c
ID ABSS5383 standard; DNA; 30 BP.
XX
AC ABSS5383;
XX
DT 16-DEC-2002 (first entry)
XX
DE Arabidopsis thaliana DNA, primer -123/-118 Fw.
XX
XX CIs control sequence; DNA damage-responder gene expression;
KW DNA damage-responder promoter; plant expression cassette;
KW transformed plant cell; primer; ss.
XX
OS Arabidopsis thaliana.
XX
PN JP2002272469-A.
XX
PD 24-SEP-2002.
XX
PF 19-MAR-2001; 2001JP-00079524.
XX
PR 19-MAR-2001; 2001JP-00079524.
XX
PA (NARA-) NARA SENTAN KAGAKU GIJUTSU DAIGAKUIN DAT.
XX
DR WPI; 2002-718706/78.
XX
PT CIs control sequence showing a capacity of controlling DNA damage-
PT responding gene expression of a higher plant, a DNA damage-responder

PT promoter, an expression cassette for a plant.
XX
PS Example 4; Page 12; 19pp; Japanese.
XX
CC The present invention relates to a cis control sequence showing a
CC capacity for controlling DNA damage-responder gene expression of a
CC higher plant, a plant (Arabidopsis thaliana) DNA damage-responder
CC promoter, and an expression cassette for a plant. The invention describes
CC an expression cassette for a plant for expressing an exotic gene, by
CC responding to DNA damage containing the above promoter and a site for
CC inserting an exotic gene, so that said exotic gene is linked to said
CC promoter expressably. Also described is a recombinant plasmid for
CC expressing an exotic gene by responding to DNA damage containing the
CC above promoter and an exotic gene linked expressably to said promoter, a
CC method for acquiring a plant cell transformed by an exotic gene wherein a
CC specific expression responding to DNA damage is desired including a step
CC of transforming a plant cell with the above recombinant plasmid to get a
CC transformed plant cell, and a transformed plant cell prepared by the
CC above method. The method is used for acquiring a plant cell transformed
CC by an exotic gene. The present sequence represents a primer used in the
CC examples of the present invention
XX
SQ Sequence 30 BP; 7 A; 6 C; 9 G; 8 T; 0 U; 0 Other;
XX
Query Match 72.0%; Score 14.4; DB 6; Length 30;
Best Local Similarity 93.8%; Pred. No. 8e+03; 1; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 4 AAAAGCTTCTTCAACA 19
Db 29 AAAGCTTCTTCAACA 14
XX
RESULT 27
ADJ66058
ID ADJ66058 standard; DNA; 33 BP.
XX
AC ADJ66058;
XX
DT 06-MAY-2004 (first entry)
XX
DE Primer 111-132.6, seq id 6.
XX
XX Transposon vector; inverted terminal repeat sequence; ITR; transposase;
KW PK08183-3; primer; ss.
XX
OS Chrysoperla carnea.
XX
PN WO2004015088-A2.
XX
PD 19-FEB-2004.
XX
PF 13-AUG-2003; 2003WO-US025364.
XX
PR 13-AUG-2002; 2002US-0403290P.
XX
PA (KOSA-) KOSAN BIOSCIENCES INC.
XX
PI Julien B;
XX
DR WPI; 2004-169502/16.
XX
PT Altering deoxyribonucleic acid in a Sorangium host cell comprises
PT transforming the host cell with a transposon vector comprising inverted
PT terminal repeat sequences (ITRs) and a gene encoding a transposase that
PT recognizes the ITRs.
XX
PS Example 2; SEQ ID NO 6; 28pp; English.
XX
CC The invention relates to a method of altering deoxyribonucleic acid (DNA)
CC in a Sorangium host cell. The method comprises transforming the host cell
CC with a transposon vector containing inverted terminal repeat sequences
CC (ITRs), and a gene encoding a transposase that recognizes the ITRs, where


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XX Mao Y, Xie Y;
PI
DR WPI; 2002-751591/82.
XX
XX Histone acetyl transferase 21.67 polypeptides and polynucleotides
PT encoding this polypeptide.
XX
XX Example 6; Page 20 (Disclosure); 33pp; Chinese.
XX
XX The invention comprises the amino acid and coding sequence of the histone
CC acetyl transferase 21.67 protein. The DNA and protein sequences of the
CC invention are useful for the treatment of malignant tumours, haemopathy,
CC HIV infection, immunological diseases and various inflammations. The
CC present DNA sequence represents a probe for the acetyl transferase 21.67
CC gene
XX
SQ Sequence 41 BP; 12 A; 13 C; 6 G; 10 T; 0 U; 0 Other;

Query Match          74.0%; Score 14.8; DB 6; Length 41;
Best Local Similarity 88.9%; Pred. No. 5.4e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 AAAAAGCTTCTTCAACAC 20
   |||||
Db 3 AAAAAGCTTATCCAACAC 20

RESULT 22
AAL51795
ID AAL51795 standard; DNA; 41 BP.
XX
XX AAL51795;
AC
XX
XX 24-APR-2003 (first entry)
DT
XX
XX Histone acetyl transferase 21-67 nucleotide probe #1.
DE
XX
XX Probe; ss; histone acetyl transferase; enzyme; 21.67; malignant tumour;
KM haemopathy; HIV; immunological disease; inflammation.
XX
XX Unidentified.
OS
XX
XX CN1361260-A.
PN
XX
XX 31-JUL-2002.
PD
XX
XX 26-DEC-2000; 2000CN-00136303.
PF
XX
XX 26-DEC-2000; 2000CN-00136303.
PR
XX
XX (BODE-) BODE GENE DEV CO LTD SHANGHAI.
PA
XX
XX Mao Y, Xie Y;
PI
XX
XX WPI; 2002-751591/82.
DR
XX
XX Histone acetyl transferase 21.67 polypeptides and polynucleotides
PT encoding this polypeptide.
XX
XX Example 6; Page 20 (Disclosure); 33pp; Chinese.
XX
XX The invention comprises the amino acid and coding sequence of the histone
CC acetyl transferase 21.67 protein. The DNA and protein sequences of the
CC invention are useful for the treatment of malignant tumours, haemopathy,
CC HIV infection, immunological diseases and various inflammations. The
CC present DNA sequence represents a probe for the acetyl transferase 21.67
CC gene
XX
SQ Sequence 41 BP; 13 A; 12 C; 6 G; 10 T; 0 U; 0 Other;

Query Match          74.0%; Score 14.8; DB 6; Length 41;
Best Local Similarity 88.9%; Pred. No. 5.4e+03;
```

```
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 AAAAAGCTTCTTCAACAC 20
   |||||
Db 3 AAAAAGCTTATCCAACAC 20

RESULT 23
ACF05858
ID ACF05858 standard; DNA; 22 BP.
XX
XX ACF05858;
AC
XX
XX 04-DEC-2003 (first entry)
DT
XX
XX Hamster INGP gene PCR primer INGEN 8_3.
DE
XX
XX Hamster; islet neogenesis gene associated protein; INGP; promoter;
KM antidiabetic; PCR; primer; ss.
XX
XX Cricetus sp.
OS
XX
XX WC2003060096-A2.
PN
XX
XX 24-JUL-2003.
PD
XX
XX 10-JAN-2003; 2003MO-US000707.
PF
XX
XX 11-JAN-2002; 2002US-0346898P.
PR
XX
XX 01-MAR-2002; 2002US-0361073P.
PR
XX
XX 14-JUN-2002; 2002US-0388315P.
XX
XX (GMPB-) GMP ENDOTHEREAPEUTICS INC.
PA
XX
XX Taylor-Fishwick D, Vinik AJ;
PI
XX
XX WPI; 2003-598524/56.
DR
XX
XX New isolated INGP nucleic acid, useful for diagnosing and treating
PT disorders associated with reduced islet cell function and/or aberrant
PT expression or activity of INGP, such as type II diabetes mellitus.
XX
XX Example 1; Page 18; 118pp; English.
XX
XX The present sequence is that of PCR primer INGEN 8_3, corresponding to
CC nucleotides 2544-2565 of the hamster islet neogenesis gene associated
CC protein (INGP) gene. It is one of a set of primers (see ACF05852-71)
CC used to generate PCR fragments of the INGP gene, which were subsequently
CC sequenced to determine the nucleotide sequence (see ACF05851) of the
CC INGP 5' regulatory region, the introns, the intron/exon junctions, and
CC the 3' polyadenylation region. The 5' regulatory region of the INGP gene
CC is susceptible to modulation by many known transcription factors, and is
CC used in claimed screening assays to identify agents capable of modulating
CC INGP gene expression. These modulating agents have potential as
CC therapeutic agents for treating type 1 and type 2 diabetes mellitus,
CC endocrine and non-endocrine hypoplasia, hypertrophy, adenoma, neoplasia
CC and nesidioblastosis
XX
XX
SQ Sequence 22 BP; 8 A; 5 C; 4 G; 5 T; 0 U; 0 Other;

Query Match          72.0%; Score 14.4; DB 9; Length 22;
Best Local Similarity 93.8%; Pred. No. 7.8e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 AAAAAGCTTCTTCAAC 18
   |||||
Db 7 AAAAAGCTCTTCAAC 22

RESULT 24
AD297756/C
ID AD297756 standard; DNA; 25 BP.
XX
```


ACK18856
ID ACK18856 standard; DNA; 25 BP.
XX
AC ACK18856;
XX
DT 14-OCT-2003 (first entry)
XX
DE Human microarray DNA oligonucleotide SEQ ID NO 118837.
XX
KW EST; ss; probe; expressed sequence tag; microarray; gene expression;
KW genetic variation; diallelic marker; polymorphism; human;
KW cross-species comparison.
XX
OS Homo sapiens.
XX
PN US2003104410-A1.
XX
PD 05-JUN-2003.
XX
PF 15-MAR-2002; 2002US-00098263.
XX
PR 16-MAR-2001; 2001US-0276759P.
XX
PA (AFPY-) APEPTOMETRIX INC.
XX
PI Miltmann MP;
XX
DR WPI; 2003-567953/53.
XX
PT New array of nucleic acid probes, useful for in situ hybridization, in
PT Southern, Northern or dot-blot hybridization to identify or detect the
PT sequence or specific mutations of any gene.
XX
PS Claim 1; SEQ ID NO 118837; 9pp; English.
XX
CC The invention discloses a microarray comprising a plurality of nucleic
CC acid probes including one of 2,018,500 fully defined sequences, or its
CC perfect match, perfect mismatch, antisense match or antisense mismatch.
CC Also disclosed is a method of gene expression analysis. The array is used
CC in monitoring gene expression levels by hybridisation to a DNA library,
CC in analysis of genetic variation or in hybridisation of tag-labelled
CC compounds. The nucleic acid probes are specifically designed for analysis
CC of at least one target sequence. The method of analysis comprises
CC hybridising at least one or more nucleic acids to at least two or more
CC nucleic acid probes and detecting the hybridisation. The nucleic acid
CC probes are attached to a solid support. The analysis comprises monitoring
CC gene expression levels, identifying diallelic markers or polymorphisms,
CC or family members of a gene and a cross-species comparison. Each of the
CC nucleic acids further comprises a tag sequence. The array of nucleic acid
CC probes is useful in situ hybridisation, in Southern, Northern or dot-
CC blot hybridisation to identify or detect the sequence or specific
CC mutations of any gene, in mapping the 5' termini of mRNA molecules by
CC primer extensions or in screening cDNA or genomic libraries or subclones
CC for additional subclones containing segments of DNA that have been
CC isolated and previously sequenced. The sequence presented is one of the
CC nucleic acid probes incorporated in the microarray. Note: The sequence
CC data for this parent can also be obtained in electronic format directly
CC from USPTO at seqdata.uspto.gov/sequence.html
XX
SQ Sequence 25 BP; 11 A; 5 C; 4 G; 5 T; 0 U; 0 Other;
XX
Query Match 74.0%; Score 14.8; DB 9; Length 25;
Best Local Similarity 88.9%; Pred. No. 5.2e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
QY 3 AAAAAGCTTCTCAACAC 20
DB 2 AAAAAGCTTCTCAACAC 19
XX
RESULT 20
AAL51793
ID AAL51793 standard; DNA; 33 BP.

XX
AC AAL51793;
XX
DT 24-APR-2003 (first entry)
XX
DE Histone acetyl transferase 21-67 PCR primer #3.
XX
KW Primer; PCR; histone acetyl transferase; enzyme; 21.67; malignant tumour;
KW haemopathy; HIV; immunological disease; inflammation; ss.
XX
OS Unidentified.
XX
PN CN1361260-A.
XX
PD 31-JUL-2002.
XX
PF 26-DEC-2000; 2000CN-00136303.
XX
PR 26-DEC-2000; 2000CN-00136303.
XX
PA (BODE-) BODE GENE DEV CO LTD SHANGHAI.
XX
PI Mao Y, Xie Y;
XX
DR WPI; 2002-751591/82.
XX
PT Histone acetyl transferase 21.67 polypeptides and polynucleotides
PT encoding this polypeptide.
XX
PS Example 4; Page 18 (Disclosure); 33pp; Chinese.
XX
CC The invention comprises the amino acid and coding sequence of the histone
CC acetyl transferase 21.67 protein. The DNA and protein sequences of the
CC invention are useful for the treatment of malignant tumours, haemopathy,
CC HIV infection, immunological diseases and various inflammations. The
CC present DNA sequence represents a PCR primer for the acetyl transferase
CC 21.67 gene
XX
SQ Sequence 33 BP; 13 A; 8 C; 5 G; 7 T; 0 U; 0 Other;
XX
Query Match 74.0%; Score 14.8; DB 6; Length 33;
Best Local Similarity 88.9%; Pred. No. 5.3e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
QY 3 AAAAAGCTTCTCAACAC 20
DB 13 AAAAAGCTTATCCAACAC 30
XX
RESULT 21
AAL51796
ID AAL51796 standard; DNA; 41 BP.
XX
AC AAL51796;
XX
DT 24-APR-2003 (first entry)
XX
DE Histone acetyl transferase 21-67 nucleotide probe #2.
XX
KW Probe; ss; histone acetyl transferase; enzyme; 21.67; malignant tumour;
KW haemopathy; HIV; immunological disease; inflammation.
XX
OS Unidentified.
XX
PN CN1361260-A.
XX
PD 31-JUL-2002.
XX
PF 26-DEC-2000; 2000CN-00136303.
XX
PR 26-DEC-2000; 2000CN-00136303.
XX
PA (BODE-) BODE GENE DEV CO LTD SHANGHAI.

Query Match 76.0%; Score 15.2; DB 5; Length 33;
Best Local Similarity 85.0%; Pred. No. 3.5e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ATAAAGCTTCTTCAAC 20
DB 13 ATGAAACCTTCTTCAAC 32

RESULT 17
ADSS3635/c
ID ADSS3635 standard; DNA; 60 BP.

AC ADSS3635;

DT 16-DEC-2004 (first entry)

DE Eucalyptus wood forming tissue expressed sequence tag #1189.

KW ss; expressed sequence tag; EST; gene expression; biosynthesis;
KW cell wall; wood fibre cell; plant; eucalyptus.

OS Eucalyptus camaldulensis.

PN WO2004081209-A1.

PD 23-SEP-2004.

PF 24-FEB-2004; 2004WO-JP002151.

PR 24-FEB-2003; 2003JP-00046427.

PA (OJIP) OJI PAPER CO.

XX Hibino T;

DR WPI; 2004-67544/66.

PT New genes specifically expressed in eucalyptus wood forming tissues,
PT useful in controlling biosynthesis of cell wall components and
PT morphological formation of wood fiber cells.

PS Claim 3; SEQ ID NO 1189; 480bp; Japanese.

CC The invention relates to a DNA (I) that shows increased or decreased
CC expression during biosynthesis of cell wall components or formation of
CC wood fibre cells in a plant, comprising a nucleotide sequence that
CC hybridises under stringent conditions with any of 1731 fully defined
CC sequences (SI) of 60 nucleotides given in specification, or with a
CC nucleotide sequence encoding a protein having 50% or more homology with
CC that encoded by (SI). Also included in the specification are: (a) a
CC promoter DNA (II) of (I); (b) a DNA comprising a nucleotide sequence that
CC is complementary to (I) or nucleotide sequence that codes RNA, which
CC suppresses the expression of (I) by RNA interference effect or the co-
CC suppressant effect; (c) a recombinant vector (III) comprising (I); (d) a
CC microorganism comprising (III); (e) a transformed plant cell (IV)
CC comprising (III); and (f) a transformed portion (V) obtained from (IV).
CC (I) are useful for regulating biosynthesis of cell wall components or
CC morphological formation of wood fibre cells. This sequence corresponds to
CC an expressed sequence tag (EST) fragment relating to the DNA of the
CC invention.

SQ Sequence 60 BP; 18 A; 9 C; 13 G; 20 T; 0 U; 0 Other;

Query Match 76.0%; Score 15.2; DB 13; Length 60;
Best Local Similarity 85.0%; Pred. No. 3.7e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ATAAAGCTTCTTCAAC 20
DB 57 ATTAAGCTTGTCAATAC 38

RESULT 18
ACK18857
ID ACK18857 standard; DNA; 25 BP.

AC ACK18857;

DT 14-OCT-2003 (first entry)

DE Human microarray DNA oligonucleotide SEQ ID NO 118838.

KW EST; ss; probe; expressed sequence tag; microarray; gene expression;
KW genetic variation; biallelic marker; polymorphism; human;
KW cross-species comparison.

OS Homo sapiens.

PN US2003104410-A1.

PD 05-JUN-2003.

PF 15-MAR-2002; 2002US-00098263.

PR 16-MAR-2001; 2001US-0276759P.

PA (AFYX-) AFFYMETRIX INC.

PI Miltenberg MP;

DR WPI; 2003-567953/53.

PT New array of nucleic acid probes, useful for in situ hybridization, in
PT Southern, Northern or dot-blot hybridization to identify or detect the
PT sequence or specific mutations of any gene.

PS Claim 1; SEQ ID NO 118838; 9pp; English.

CC The invention discloses a microarray comprising a plurality of nucleic
CC acid probes including one of 2,018,500 fully defined sequences, or its
CC perfect match, perfect mismatch, antisense match or antisense mismatch.
CC Also disclosed is a method of gene expression analysis. The array is used
CC in monitoring gene expression levels by hybridisation to a DNA library,
CC in analysis of genetic variation or in hybridisation of tag-labelled
CC compounds. The nucleic acid probes are specifically designed for analysis
CC of at least one target sequence. The method of analysis comprises
CC hybridising at least one or more nucleic acids to at least two or more
CC nucleic acid probes and detecting the hybridisation. The nucleic acid
CC probes are attached to a solid support. The analysis comprises monitoring
CC gene expression levels, identifying biallelic markers or polymorphisms,
CC or family members of a gene and a cross-species comparison. Each of the
CC nucleic acids further comprises a tag sequence. The array of nucleic acid
CC probes is useful in in situ hybridisation, in Southern, Northern or dot-
CC blot hybridisation to identify or detect the sequence or specific
CC mutations of any gene, in mapping the 5' terminus of mRNA molecules by
CC primer extensions or in screening cDNA or genomic libraries or subclones
CC for additional subclones containing segments of DNA that have been
CC isolated and previously sequenced. The sequence presented is one of the
CC nucleic acid probes incorporated in the microarray. Note: The sequence
CC data for this patent can also be obtained in electronic format directly
CC from USPTO at seqdata.uspto.gov/sequence.html

SQ Sequence 25 BP; 11 A; 4 C; 5 G; 5 T; 0 U; 0 Other;

Query Match 74.0%; Score 14.8; DB 9; Length 25;
Best Local Similarity 88.9%; Pred. No. 5.2e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 AAAAGCTTCTTCAAC 20
DB 2 AAAAGCTTCTGCAAGAC 19

RESULT 19

PS Claim 11; Col 39; 31pp; English.

XX Sequences AAA06974-A07013 represent antisense oligonucleotides targeted

CC to the human Smad5 gene, which inhibit its expression. The antisense

CC oligonucleotides were designed to target different regions of the human

CC Smad5 RNA, and were analyzed for their effect on Smad5 mRNA levels by

CC quantitative real-time PCR. The Smad proteins are a family of cytosolic

CC proteins which are involved in TGF-beta superfamily signal transduction.

CC On ligand binding, TGF-beta superfamily proteins (such as bone

CC morphogenetic protein (BMP), activin and TGF-betas themselves)

CC phosphorylate Smad proteins, which then homo- or heterodimerize and

CC translocate to the nucleus to activate target gene transcription. Smad5

CC (also known as MADH5, Dwarin-C and V5-1) is a member of the subgroup of

CC Smad family transcription factors which mediate signal transduction from

CC BMPs. Smad5 is activated by BMP-2 through the BMP type Ia or Ib

CC receptors, causing it to heterodimerize with the common mediator Smad4

CC (US6013787; AAY69622) and translocate to the nucleus. The antisense

CC oligonucleotides of the invention are useful for diagnosis, prevention

CC and treatment of conditions associated with Smad5 expression, such as

CC tumour formation, inflammation and certain infections

CC XX

SQ Sequence 18 BP; 7 A; 6 C; 2 G; 3 T; 0 U; 0 Other;

Query Match 77.0%; Score 15.4; DB 3; Length 18;

Best Local Similarity 94.1%; Pred. No. 2.7e+03;

Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 4 AAAAGCTTCTCAACAC 20

Db 2 AAAAGCTTCTCAACAC 18

|||||

RESULT 15

AAA89127

ID AAA89127 standard; DNA; 33 BP.

XX AAA89127;

AC 19-MAR-2001 (first entry)

DT XX

DB Neisseria ORF4 lipoprotein PCR primer orf4-L for.

KM Neisseria meningitidis; Neisseria gonorrhoeae; ORF4; lipoprotein;

KW infection; diagnosis; therapy; vaccine; PCR primer; ss.

XX

OS Neisseria sp.

XX WO200071725-A2.

FN 30-NOV-2000.

XX

PD 19-MAY-2000; 2000MO-IB000828.

XX

PF 19-MAY-1999; 99GB-00011692.

PR 19-AUG-1999; 99GB-00019705.

PR 09-MAR-2000; 2000GB-00005730.

XX

PA (CHIR-) CHIRON SPA.

XX

PI Giuliani MM, Pizsa M, Rappuoli R;

XX WPI; 2001-025167/03.

DR

XX

PT Novel composition comprising first and second biological molecules from a

PT Neisseria bacterium, useful as vaccines or immunogenic compositions for

PT treating Neisserial infections.

XX

XX Example 4; Page 60; 126pp; English.

PS

CC This oligonucleotide, termed orf4-L for, is used as forward primer, with

CC the reverse primer given in AAA89128, for the PCR amplification of ORF4

CC lipoprotein of a Neisseria sp. The PCR product was used in expression and

CC purification experiments, and can be used as 1 component of novel

CC combination compositions of the invention. These compositions comprise:

CC (i) 2 or more Neisserial proteins, (ii) 2 or more different Neisserial

CC nucleic acids; or (iii) mixtures of 1 or more Neisserial protein and 1 or

CC more Neisserial nucleic acid. The proteins and nucleic acids are

CC preferably from different Neisseria spp., especially Neisseria

CC meningitidis and Neisseria gonorrhoeae, but may be from the same species,

CC or from different serogroups or strains of the same species. The

CC compositions are used e.g. as immunogenic compositions, vaccines or

CC diagnostic reagents. They are used to treat or prevent Neisserial

CC infection, to detect the presence of Neisserial bacteria or of antibodies

CC raised against Neisserial bacteria, and/or as reagents which can raise

CC antibodies against Neisserial bacteria

CC XX

SQ Sequence 33 BP; 11 A; 11 C; 4 G; 7 T; 0 U; 0 Other;

Query Match 76.0%; Score 15.2; DB 5; Length 33;

Best Local Similarity 85.0%; Pred. No. 3.5e+03;

Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 ATAAAAGCTTCTCAACAC 20

Db 13 ATGAAAAGCTTCTCAAAAC 32

|||||

RESULT 16

AAS43911

ID AAS43911 standard; DNA; 33 BP.

XX AAS43911;

AC 18-DEC-2001 (first entry)

DT XX

DE Neisseria meningitidis B MC58 genomic DNA sequence PCR primer #6.

XX

DE Neisseria gonorrhoeae; leader peptide; fusion protein; ORF46.1; ss;

KM Neisserial protein; PCR primer.

KW

XX

OS Neisseria meningitidis.

OS Synthetic.

XX

PN WO200164922-A2.

XX

PD 07-SEP-2001.

XX

PF 28-FEB-2001; 2001WO-IB000452.

XX

PR 28-FEB-2000; 2000GB-00004695.

PR 13-NOV-2000; 2000GB-00027675.

XX

PA (CHIR-) CHIRON SPA.

XX

PI Arico MB, Comanducci M, Galeotti C, Massignani V, Giuliani MM;

PI Pizsa M;

XX

DR WPI; 2001-582163/65.

XX

PT Producing heterologous proteins from Neisseria meningitidis and N.

PT gonorrhoeae.

XX

PS Disclosure; Page 81; 119pp; English.

XX

XX The invention relates to methods for the heterologous expression of

CC Neisserial proteins from Neisseria meningitidis and Neisseria

CC gonorrhoeae. At least one domain in the protein is deleted, e.g. the

CC leader peptide, and may be replaced by a domain from a different protein

CC to make a fusion protein, in order to enhance heterologous expression of

CC Neisserial proteins. Also, a region of a protein, such as a poly-glycine

CC stretch, can be mutated to enhance expression. The proteins used in the

CC processes include ORF46.1, 287, 741, 919, 953, 961 and 983. Sequences

CC AAS43807-AAS43867 and AAS43906-AAS44358 represent PCR primers used in the

CC methods of the invention

XX

SQ Sequence 33 BP; 11 A; 11 C; 4 G; 7 T; 0 U; 0 Other;

```
XX AEA02855;
AC
XX
XX 28-JUL-2005 (first entry)
DT
XX
XX Bacillus PCR primer SEQ ID NO 98.
DE
XX
XX ss; PCR; food; antibiotic; sugar; primer.
KM
XX
XX Bacillus sp.
OS
XX
XX WO2005045013-A2.
PN
XX
XX 19-MAY-2005.
PD
XX
XX 05-NOV-2004; 2004WO-JP016891.
PF
XX
XX 07-NOV-2003; 2003JP-00379167.
PR
XX
XX (KAOS ) KAO CORP.
PA
XX
XX Tohata M, Sawada K, Ozaki K, Kobayashi K, Ogasawara N;
PI
XX
XX WPI; 2005-347061/35.
DR
XX
XX New recombinant microorganism of genus Bacillus, useful for producing a
PT
XX
XX protein of interest or substances, e.g. food, antibiotics, sugars, or
PT
XX
XX lipids.
XX
XX Example 1; SEQ ID NO 98; 62pp; English.
PS
XX
XX The invention relates to a recombinant microorganism prepared by
CC
XX
XX transferring, to a mutant strain of microorganism from which any of
CC
XX
XX Bacillus subtilis genes have been deleted or knocked out, a gene encoding
CC
XX
XX a heterologous protein or polypeptide. The recombinant microorganism and
CC
XX
XX method are useful for producing a protein or polypeptide of interest or
CC
XX
XX substances, e.g. food, antibiotics, sugars, or lipids. The present
CC
XX
XX sequence represents a Bacillus PCR primer.
XX
XX
SQ Sequence 45 BP; 17 A; 12 C; 3 G; 13 T; 0 U; 0 Other;

Query Match 82.0%; Score 16.4; DB 14; Length 45;
Best Local Similarity 94.4%; Pred. No. 1e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AATAAAGCTTCTTCAAC 18
DB 24 AATAAAGCTTCTTCAAC 41

RESULT 13
ADK67815
ID ADK67815 standard; DNA; 33 BP.
XX
XX ADK67815;
AC
XX
XX 06-MAY-2004 (first entry)
DT
XX
XX Francisella tularensis hybridisation probe.
DE
XX
XX Francisella tularensis biological weapon; detection; probe; ss.
KM
XX
XX Francisella tularensis.
OS
XX
XX WO2004013357-A2.
PN
XX
XX 12-FEB-2004.
PD
XX
XX 31-JUL-2003; 2003WO-US024218.
PF
XX
XX 01-AUG-2002; 2002US-0400892P.
PR
XX
XX 29-JUL-2003; 2003US-00630154.
XX
```

```
PA (REGC ) UNIV CALIFORNIA.
XX
XX McCreedy PM, Radnedge L, Andersen GL, Ott LL, Slezak TR;
PI
XX
XX Kuczmarski TA, Vitalis EA;
PI
XX
XX WPI; 2004-157139/15.
DR
XX
XX New composition comprising an Amplicon that is a single strand sequence
PT
XX
XX of nucleic acids specific to Francisella tularensis, useful for detecting
PT
XX
XX Francisella tularensis.
XX
XX Claim 3; SEQ ID NO 31; 29pp; English.
PS
XX
XX The present sequence is that of a hybridisation probe for a specific
CC
XX
XX Francisella tularensis nucleotide sequence ADK67816 that serves as a
CC
XX
XX marker or signature for identification of the bacterium. F. tularensis is
CC
XX
XX the causative agent of tularemia and a potential weapon of mass
CC
XX
XX destruction and instrument of terror. A PCR forward primer ADK67813,
CC
XX
XX reverse primer ADK67814 and the present hybridisation probe can be used
CC
XX
XX to detect the specific F. tularensis nucleotide sequence, especially
CC
XX
XX using a fluorogenic 5' nuclease PCR assay. The invention provides
CC
XX
XX different primer/probe sets for different loci on the F. tularensis
CC
XX
XX genome. Also provided is a method for identifying F. tularensis by
CC
XX
XX analysing samples taken from monitoring devices, such as air monitors,
CC
XX
XX for nucleotide sequences that are specific to the bacterium. As the
CC
XX
XX nucleotide sequences are unique to F. tularensis, the primers/probes
CC
XX
XX provide a more reliable method of detection than existing methods,
CC
XX
XX reducing the occurrence of false positive and false negative results.
XX
XX
SQ Sequence 33 BP; 10 A; 8 C; 5 G; 10 T; 0 U; 0 Other;

Query Match 79.0%; Score 15.8; DB 12; Length 33;
Best Local Similarity 89.5%; Pred. No. 1.9e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AATAAAGCTTCTTCAACA 19
DB 13 ATCAGAGCTTCTTCAACA 31

RESULT 14
AAA07003
ID AAA07003 standard; DNA; 18 BP.
XX
XX AAA07003;
AC
XX
XX 03-JUL-2000 (first entry)
DT
XX
XX Human Smads phosphorothioate antisense oligonucleotide, SEQ ID NO:37.
DE
XX
XX Smads; MADH5; Dwarfin-C; JVS-1; TGF-beta signalling pathway;
KM
XX
XX transcription factor; expression inhibition; tumour formation;
KM
XX
XX inflammation; antisense; ss.
XX
XX Homo sapiens.
OS
XX
XX US6040178-A.
PN
XX
XX 21-MAR-2000.
PD
XX
XX 23-FEB-1999; 99US-00256492.
PF
XX
XX 23-FEB-1999; 99US-00256492.
PR
XX
XX (ISIS-) ISIS PHARM INC.
PA
XX
XX Monia BP, Cowsett LM;
PI
XX
XX WPI; 2000-270139/23.
XX
XX Novel antisense compounds useful for inhibiting the expression of Smads
PT
XX
XX in human cells or tissues and treating inflammation and tumor formation.
XX
```

```
PD 19-MAY-2005.
XX
XX 05-NOV-2004; 2004WO-JP016891.
PF
XX 07-NOV-2003; 2003JP-00379167.
PR
XX (KAOS ) KAO CORP.
PA
XX Tohata M, Sawada K, Ozaki K, Kobayashi K, Ogasawara N;
XX WPI; 2005-347061/35.
DR
XX
XX New recombinant microorganism of genus Bacillus, useful for producing a
PT protein of interest or substances, e.g. food, antibiotics, sugars, or
PT lipids.
XX
XX Example 1; SEQ ID NO 118; 62pp; English.
PS
XX The invention relates to a recombinant microorganism prepared by
CC transferring, to a mutant strain of microorganism from which any of
CC Bacillus subtilis genes have been deleted or knocked out, a gene encoding
CC a heterologous protein or polypeptide. The recombinant microorganism and
CC method are useful for producing a protein or polypeptide of interest or
CC substances, e.g. food, antibiotics, sugars, or lipids. The present
CC sequence represents a Bacillus PCR primer.
XX
SQ Sequence 45 BP; 14 A; 10 C; 5 G; 16 T; 0 U; 0 Other;

Query Match 82.0%; Score 16.4; DB 14; Length 45;
Best Local Similarity 94.4%; Pred. No. 1e+03; 1; Indels 0; Gaps 0;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATAAAGCTTCTTCAAC 18
    ||||| ||||| |||||
Db 24 ATAAAGCTTCTTCAAC 41

RESULT 10
AEA02869
ID AEA02869 standard; DNA; 45 BP.
XX
XX AEA02869;
AC
XX 28-JUL-2005 (first entry)
DT
XX
XX Bacillus PCR primer SEQ ID NO 112.
DE
XX ss; PCR; food; antibiotic; sugar; primer.
KM
XX Bacillus sp.
OS
XX WO2005045013-A2.
PN
XX 19-MAY-2005.
PD
XX 05-NOV-2004; 2004WO-JP016891.
PF
XX 07-NOV-2003; 2003JP-00379167.
PR
XX (KAOS ) KAO CORP.
PA
XX Tohata M, Sawada K, Ozaki K, Kobayashi K, Ogasawara N;
XX WPI; 2005-347061/35.
DR
XX
XX New recombinant microorganism of genus Bacillus, useful for producing a
PT protein of interest or substances, e.g. food, antibiotics, sugars, or
PT lipids.
XX
XX Example 1; SEQ ID NO 112; 62pp; English.
PS
XX The invention relates to a recombinant microorganism prepared by
CC transferring, to a mutant strain of microorganism from which any of
```

```
CC Bacillus subtilis genes have been deleted or knocked out, a gene encoding
CC a heterologous protein or polypeptide. The recombinant microorganism and
CC method are useful for producing a protein or polypeptide of interest or
CC substances, e.g. food, antibiotics, sugars, or lipids. The present
CC sequence represents a Bacillus PCR primer.
XX
SQ Sequence 45 BP; 18 A; 11 C; 4 G; 12 T; 0 U; 0 Other;

Query Match 82.0%; Score 16.4; DB 14; Length 45;
Best Local Similarity 94.4%; Pred. No. 1e+03; 1; Indels 0; Gaps 0;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATAAAGCTTCTTCAAC 18
    ||||| ||||| |||||
Db 24 ATAAAGCTTCTTCAAC 41

RESULT 11
AEA02849
ID AEA02849 standard; DNA; 45 BP.
XX
XX AEA02849;
AC
XX 28-JUL-2005 (first entry)
DT
XX
XX Bacillus PCR primer SEQ ID NO 92.
DE
XX ss; PCR; food; antibiotic; sugar; primer.
KM
XX Bacillus sp.
OS
XX WO2005045013-A2.
PN
XX 19-MAY-2005.
PD
XX 05-NOV-2004; 2004WO-JP016891.
PF
XX 07-NOV-2003; 2003JP-00379167.
PR
XX (KAOS ) KAO CORP.
PA
XX Tohata M, Sawada K, Ozaki K, Kobayashi K, Ogasawara N;
XX WPI; 2005-347061/35.
DR
XX
XX New recombinant microorganism of genus Bacillus, useful for producing a
PT protein of interest or substances, e.g. food, antibiotics, sugars, or
PT lipids.
XX
XX Example 1; SEQ ID NO 92; 62pp; English.
PS
XX The invention relates to a recombinant microorganism prepared by
CC transferring, to a mutant strain of microorganism from which any of
CC Bacillus subtilis genes have been deleted or knocked out, a gene encoding
CC a heterologous protein or polypeptide. The recombinant microorganism and
CC method are useful for producing a protein or polypeptide of interest or
CC substances, e.g. food, antibiotics, sugars, or lipids. The present
CC sequence represents a Bacillus PCR primer.
XX
SQ Sequence 45 BP; 19 A; 11 C; 8 G; 7 T; 0 U; 0 Other;

Query Match 82.0%; Score 16.4; DB 14; Length 45;
Best Local Similarity 94.4%; Pred. No. 1e+03; 1; Indels 0; Gaps 0;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATAAAGCTTCTTCAAC 18
    ||||| ||||| |||||
Db 16 ATAAAGCTTCTTCAAC 33

RESULT 12
AEA02855
ID AEA02855 standard; DNA; 45 BP.
```

```
RESULT 7
ADN49096/c
ID ADN49096 standard; DNA; 20 BP.
XX
AC ADN49096;
XX
DT 15-JUL-2004 (first entry)
XX
DE Human histone deacetylase 2 (HDAC2) DNA target region #20.
XX
KM Histone deacetylase 2; HDAC2; HDAC2; hdac2; RPD3; hRPD3;
KW hyperproliferative disorder; cancer; antisense gene therapy; human; ds;
XX chromosome 6q21.
XX
OS Homo sapiens.
XX
PN US200407578-A1.
XX
PD 22-APR-2004.
XX
PF 02-SEP-2003; 2003US-00653528.
XX
PR 14-JUN-2002; 2002US-00173192.
XX
PA (MONT/) MONTA B P.
PA (DOBI/) DOBIE K W.
XX
PI Monia BP, Dobie KW;
XX
DR WPI; 2004-340037/31.
XX
PT New compound, having a sequence targeted to a coding region of a nucleic
PT acid encoding human histone deacetylase 2, useful for preparing a
PT composition for treating hyperproliferative disorders, e.g., cancer.
XX
PS Example 15; SEQ ID NO 67; 47pp; English.
XX
XX The invention relates to antisense compounds, compositions and methods
CC for modulating the expression of histone deacetylase 2 (HDAC2). HDAC2 is
CC also known as HDAC-2, hdac2, human RPD3 and hRPD3. The composition
CC comprises antisense compounds that can be targeted towards HDAC2. The
CC compound is useful for preparing a composition for treating
CC hyperproliferative disorders, e.g., cancer. It is also useful in
CC antisense gene therapy. The present sequence is human HDAC2 DNA target
CC region. Human HDAC2 gene is located at chromosome 6q21.
XX
SQ Sequence 20 BP; 5 A; 1 C; 6 G; 8 T; 0 U; 0 Other;
Query Match 85.0%; Score 17; DB 12; Length 20;
Best Local Similarity 100.0%; Pred. No. 5e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 AAAAGCTTCTTCAACAC 20
DB 20 AAAAGCTTCTTCAACAC 4
RESULT 8
ADN49072
ID ADN49072 standard; DNA; 20 BP.
XX
AC ADN49072;
XX
DT 15-JUL-2004 (first entry)
XX
DE Human HDAC2 specific antisense oligo, ISIS 157274.
XX
KM Histone deacetylase 2; HDAC2; HDAC-2; hdac2; RPD3; hRPD3;
KW hyperproliferative disorder; cancer; antisense gene therapy; human;
XX antisense; phosphorothioate backbone; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
```

```
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= b
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone in which all cytidines
FT are 5-methylcytidines"
FT modified_base 1..5
FT /*tag= a
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl bases"
FT modified_base 16..20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl bases"
XX
PN US200407578-A1.
XX
PD 22-APR-2004.
XX
PF 02-SEP-2003; 2003US-00653528.
XX
PR 14-JUN-2002; 2002US-00173192.
XX
PA (MONT/) MONTA B P.
PA (DOBI/) DOBIE K W.
XX
PI Monia BP, Dobie KW;
XX
DR WPI; 2004-340037/31.
XX
PT New compound, having a sequence targeted to a coding region of a nucleic
PT acid encoding human histone deacetylase 2, useful for preparing a
PT composition for treating hyperproliferative disorders, e.g., cancer.
XX
PS Example 15; SEQ ID NO 43; 47pp; English.
XX
XX The invention relates to antisense compounds, compositions and methods
CC for modulating the expression of histone deacetylase 2 (HDAC2). HDAC2 is
CC also known as HDAC-2, hdac2, human RPD3 and hRPD3. The composition
CC comprises antisense compounds that can be targeted towards HDAC2. The
CC compound is useful for preparing a composition for treating
CC hyperproliferative disorders, e.g., cancer. It is also useful in
CC antisense gene therapy. The present sequence is an antisense
CC oligonucleotide targeted to human HDAC2 DNA.
XX
SQ Sequence 20 BP; 8 A; 6 C; 1 G; 5 T; 0 U; 0 Other;
Query Match 85.0%; Score 17; DB 12; Length 20;
Best Local Similarity 100.0%; Pred. No. 5e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 AAAAGCTTCTTCAACAC 20
DB 1 AAAAGCTTCTTCAACAC 17
RESULT 9
AEA02875
ID AEA02875 standard; DNA; 45 BP.
XX
AC AEA02875;
XX
DT 28-JUL-2005 (first entry)
XX
DE Bacillus PCR primer SEQ ID NO 118.
XX
KM ss; PCR; food; antibiotic; sugar; primer.
XX
KW Bacillus sp.
OS
XX
PN WO2005045013-A2.
XX
```

CC for gene silencing by RNA interference.
XX Sequence 19 BP; 9 A; 5 C; 1 G; 0 T; 4 U; 0 Other;

Query Match 87.0%; Score 17.4; DB 14; Length 19;
Best Local Similarity 73.7%; Pred. No. 3.3e+02;
Matches 14; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 2 TAAAGCTTCTCAACAC 20
Db 1 UAAAGCAUCUCCACAC 19

RESULT 5

ADJ27026
ID ADJ27026 standard; DNA; 20 BP.

AC ADJ27026;

XX 20-MAY-2004 (first entry)

DE Human histone deacetylase 2 DNA antisense oligo, ISIS #157274.

XX Histone deacetylase 2; HDAC2; diagnosis; prevention;
KM hyperproliferative disorder; cancer; apoptosis; metabolic disorder;
KW antisense-therapy; cytostatic; antiinflammatory; human;
KM phosphorothioate backbone; antisense; ss.

XX Homo sapiens.
OS Synthetic.

XX Key location/Qualifiers

FT modified_base 1..20

FT /tag= b

FT /mod_base= OTHER

FT /note= "Phosphorothioate backbone where all cyridines are

FT modified_base 1..5

FT /tag= a

FT /mod_base= OTHER

FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"

FT modified_base 16..20

FT /tag= c

FT /mod_base= OTHER

FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"

FT US2003236204-A1.

XX 25-DEC-2003.

XX 14-JUN-2002; 2002US-00173192.

XX 14-JUN-2002; 2002US-00173192.

XX (ISIS-) ISIS PHARM INC.

XX Monia BP, Dobie KM;

XX WPI; 2004-070606/07.

XX New antisense oligonucleotide compound, useful for diagnosing, preventing

XX and/or treating conditions with aberrant activity of the histone

XX deacetylase 2, such as cancer, inflammation and metabolic disorders.

XX Example 15; SEQ ID NO 43; 46bp; English.

XX The present invention relates to antisense compounds, compositions and
XX methods used for modulating histone deacetylase 2 (HDAC2). The methods
XX and compositions are useful for the diagnosis, prevention and/or treatment of diseases or conditions associated with
XX aberrant expression or activity of histone deacetylase 2, such as a
XX hyperproliferative disorder (cancer), a condition involving an
XX inflammatory response or an aberrant apoptosis and a metabolic disorder.

CC The invention is also useful in antisense-therapy. The present sequence
CC is human histone deacetylase 2 DNA antisense oligonucleotide used in the
CC exemplification of the invention.

XX Sequence 20 BP; 8 A; 6 C; 1 G; 5 T; 0 U; 0 Other;

Query Match 85.0%; Score 17; DB 12; Length 20;
Best Local Similarity 100.0%; Pred. No. 5e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 AAAAGCTTCTCAACAC 20
Db 1 AAAAGCTTCTCAACAC 17

RESULT 6

ADJ27050/c
ID ADJ27050 standard; DNA; 20 BP.

AC ADJ27050;

XX 20-MAY-2004 (first entry)

DE Human histone deacetylase 2 target DNA fragment #20.

XX Histone deacetylase 2; HDAC2; diagnosis; prevention;
KM hyperproliferative disorder; cancer; apoptosis; metabolic disorder;
KW antisense-therapy; cytostatic; antiinflammatory; human; ds.

XX Homo sapiens.
OS Synthetic.

XX US2003236204-A1.

XX 25-DEC-2003.

XX 14-JUN-2002; 2002US-00173192.

XX 14-JUN-2002; 2002US-00173192.

XX (ISIS-) ISIS PHARM INC.

XX Monia BP, Dobie KM;

XX WPI; 2004-070606/07.

XX New antisense oligonucleotide compound, useful for diagnosing, preventing

XX and/or treating conditions with aberrant activity of the histone

XX deacetylase 2, such as cancer, inflammation and metabolic disorders.

XX Example 15; SEQ ID NO 67; 46bp; English.

XX The present invention relates to antisense compounds, compositions and
XX methods used for modulating histone deacetylase 2 (HDAC2). The methods
XX and compositions are useful for the diagnosis, prevention and/or treatment of diseases or conditions associated with
XX aberrant expression or activity of histone deacetylase 2, such as a
XX hyperproliferative disorder (cancer), a condition involving an
XX inflammatory response or an aberrant apoptosis and a metabolic disorder.

XX The invention is also useful in antisense-therapy. The present sequence
XX is human histone deacetylase 2 target DNA fragment used in the
XX exemplification of the invention.

XX Sequence 20 BP; 5 A; 1 C; 6 G; 8 T; 0 U; 0 Other;

Query Match 85.0%; Score 17; DB 12; Length 20;
Best Local Similarity 100.0%; Pred. No. 5e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 AAAAGCTTCTCAACAC 20
Db 20 AAAAGCTTCTCAACAC 4

CC hyperproliferative disorders, e.g., cancer. It is also useful in
CC antisense gene therapy. The present sequence is an antisense
CC oligonucleotide targeted to human HDAC2 DNA.
XX
SQ Sequence 20 BP; 9 A; 5 C; 1 G; 5 T; 0 U; 0 Other;
Query Match 100.0%; Score 20; DB 12; Length 20;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATAAAGCTTCTCAACAC 20
DB 1 ATAAAGCTTCTCAACAC 20
RESULT 3
ADZ78744/c
ID ADZ78744 standard; RNA; 19 BP.
XX
AC ADZ78744;
XX
DT 14-JUL-2005 (first entry)
XX
DE N-Ras siRNA target sequence SEQ ID NO 254.
XX
KW cytostatic; gene therapy; gene expression; RNA interference;
KW antisense therapy; cancer; cytostatic; neoplasm; hyperproliferation;
KW N-Ras; ss.
XX
OS Homo sapiens.
XX
PN WO2005040379-A2.
XX
PD 06-MAY-2005.
XX
PF 20-AUG-2004; 2004WO-US027333.
XX
PR 23-OCT-2003; 2003US-00693059.
PR 24-NOV-2003; 2003US-00720448.
PR 03-DEC-2003; 2003US-00727780.
PR 14-JAN-2004; 2004US-00757803.
PR 10-FEB-2004; 2004US-0543480P.
PR 13-FEB-2004; 2004US-00780447.
PR 16-APR-2004; 2004US-00826966.
PR 30-APR-2004; 2004WO-US013456.
PR 24-MAY-2004; 2004WO-US016390.
XX
PA (SIRN-) SIRNA THERAPEUTICS INC.
XX
PI Mcswigen J;
XX
PI MPI; 2005-333508/34.
XX
DR
XX
PT New chemically synthesized double stranded short interfering nucleic acid
PT molecule that directs cleavage of N-RAS RNA via RNA interference, useful
PT for modulating RAS gene expression.
XX
PS Claim 33; SEQ ID NO 254; 204bp; English.
XX
XX The invention describes a chemically synthesized double stranded short
XX interfering nucleic acid (siNA) molecule (I) that directs cleavage of a N
XX -RAS RNA via RNA interference (RNAi), where each strand of the siNA
XX molecule is 18-23 nucleotides in length, and one strand of the siNA
XX molecule comprises nucleotide sequence complementary to the N-RAS RNA for
XX the siNA molecule to direct cleavage of the N-RAS RNA via RNA
XX interference. Also disclosed are an expression vector comprising a
XX nucleic acid sequence encoding an siNA molecule; and a mammalian cell
XX comprising the expression vector. The siNA molecule (I) is useful for
XX modulating RAS gene expression. It is also useful for modulating the
XX expression and activity of other genes in the pathways of RAS. The siNA
XX molecule is also useful for diagnosing or treating diseases and
XX conditions that respond to the modulation of RAS gene expression or
XX activity, e.g. cancer or other proliferative diseases, disorders, or

CC conditions. This sequence represents a human N-Ras siRNA target sequence
CC for gene silencing by RNA interference.
XX
SQ Sequence 19 BP; 4 A; 1 C; 5 G; 0 T; 9 U; 0 Other;
Query Match 87.0%; Score 17.4; DB 14; Length 19;
Best Local Similarity 94.7%; Pred. No. 3.3e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2 TAAAGCTTCTCAACAC 20
DB 19 TAAAGCTTCTCAACAC 1
RESULT 4
ADZ78853
ID ADZ78853 standard; RNA; 19 BP.
XX
AC ADZ78853;
XX
DT 14-JUL-2005 (first entry)
XX
DE N-Ras siRNA target sequence SEQ ID NO 363.
XX
KW cytostatic; gene therapy; gene expression; RNA interference;
KW antisense therapy; cancer; cytostatic; neoplasm; hyperproliferation;
KW N-Ras; ss.
XX
OS Homo sapiens.
XX
PN WO2005040379-A2.
XX
PD 06-MAY-2005.
XX
PF 20-AUG-2004; 2004WO-US027333.
XX
PR 23-OCT-2003; 2003US-00693059.
PR 24-NOV-2003; 2003US-00720448.
PR 03-DEC-2003; 2003US-00727780.
PR 14-JAN-2004; 2004US-00757803.
PR 10-FEB-2004; 2004US-0543480P.
PR 13-FEB-2004; 2004US-00780447.
PR 16-APR-2004; 2004US-00826966.
PR 30-APR-2004; 2004WO-US013456.
PR 24-MAY-2004; 2004WO-US016390.
XX
PA (SIRN-) SIRNA THERAPEUTICS INC.
XX
PI Mcswigen J;
XX
PI MPI; 2005-333508/34.
XX
DR
XX
PT New chemically synthesized double stranded short interfering nucleic acid
PT molecule that directs cleavage of N-RAS RNA via RNA interference, useful
PT for modulating RAS gene expression.
XX
PS Claim 33; SEQ ID NO 363; 204bp; English.
XX
XX The invention describes a chemically synthesized double stranded short
XX interfering nucleic acid (siNA) molecule (I) that directs cleavage of a N
XX -RAS RNA via RNA interference (RNAi), where each strand of the siNA
XX molecule is 18-23 nucleotides in length, and one strand of the siNA
XX molecule comprises nucleotide sequence complementary to the N-RAS RNA for
XX the siNA molecule to direct cleavage of the N-RAS RNA via RNA
XX interference. Also disclosed are an expression vector comprising a
XX nucleic acid sequence encoding an siNA molecule; and a mammalian cell
XX comprising the expression vector. The siNA molecule (I) is useful for
XX modulating RAS gene expression. It is also useful for modulating the
XX expression and activity of other genes in the pathways of RAS. The siNA
XX molecule is also useful for diagnosing or treating diseases and
XX conditions that respond to the modulation of RAS gene expression or
XX activity, e.g. cancer or other proliferative diseases, disorders, or
XX conditions. This sequence represents a human N-Ras siRNA target sequence

93	14	70.0	34	6	AAL50959	AAL50959 DNA polym
94	14	70.0	34	6	ABV76620	ABV76620 L2 motif
95	14	70.0	34	6	AAf88890	AAf88890 Human rib
96	14	70.0	34	6	ABA05115	ABA05115 Human DNA
97	14	70.0	34	6	AAL50861	AAL50861 Human 32-
98	14	70.0	34	6	ABV74749	ABV74749 Histidino
99	14	70.0	34	6	ABV74793	ABV74793 Ribosomal
100	14	70.0	34	6	ABV76335	ABV76335 Hydrogen

ALIGNMENTS

```

RESULT 1
ADJ27015
ID ADJ27015 standard; DNA; 20 BP.
XX
AC ADJ27015;
XX
DT 20-MAY-2004 (first entry)
XX
DE Human histone deacetylase 2 DNA antisense oligo, ISIS #157263.
XX
KM Histone deacetylase 2; HDAC2; diagnosis; prevention;
KM hyperproliferative disorder; cancer; apoptosis; metabolic disorder;
KM antisense-therapy; cytostatic; antiinflammatory; human;
KM phosphorothioate backbone; antisense; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key
FH modified_base
FT 1..20
FT /tag= b
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone where all cytidines are
FT 5-methyl cytidines"
FT 1..5
FT /tag= a
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"
FT 16..20
FT /tag= c
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"
XX
XX US2003236204-A1.
XX
XX 25-DEC-2003.
XX
XX 14-JUN-2002; 2002US-00173192.
XX
XX 14-JUN-2002; 2002US-00173192.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Monia BP, Dobie KM;
XX
XX WPI, 2004-070606/07.
XX
XX New antisense oligonucleotide compound, useful for diagnosing, preventing
XX and/or treating conditions with aberrant activity of the histone
XX deacetylase 2, such as cancer, inflammation and metabolic disorders.
XX
XX Example 15; SEQ ID NO 32; 46pp; English.
XX
XX The present invention relates to antisense compounds, compositions and
XX methods used for modulating histone deacetylase 2 (HDAC2). The methods
XX and compositions of the present invention are useful for the diagnosis,
XX prevention and/or treatment of diseases or conditions associated with
XX aberrant expression or activity of histone deacetylase 2, such as a
XX hyperproliferative disorder (cancer), a condition involving an
XX inflammatory response or an aberrant apoptosis and a metabolic disorder.

```

CC The invention is also useful in antisense-therapy. The present sequence
 CC is human histone deacetylase 2 DNA antisense oligonucleotide used in the
 CC exemplification of the invention.

XX Sequence 20 BP; 9 A; 5 C; 1 G; 5 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 12; Length 20;

Best Local Similarity 100.0%; Pred. No. 21; Mismatches 0; Gaps 0;

Matches 20; Conservative 0; Indels 0; Gaps 0;

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OY 1 ATAAAAGCTTCTTCAACAC 20
Db 1 ATAAAAGCTTCTTCAACAC 20

```

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RESULT 2
ADN49061
ID ADN49061 standard; DNA; 20 BP.
XX
AC ADN49061;
XX
DT 15-JUN-2004 (first entry)
XX
DE Human HDAC2 specific antisense oligo, ISIS 157263.
XX
KM Histone deacetylase 2; HDAC2; HDAC-2; hdac2; RPD3; hRPD3;
KM hyperproliferative disorder; cancer; antisense gene therapy; human;
KM antisense; phosphorothioate backbone; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key
FH modified_base
FT 1..20
FT /tag= b
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone in which all cytidines
FT are 5-methylcytidines"
FT 1..5
FT /tag= a
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl bases"
FT 16..20
FT /tag= c
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl bases"
XX
XX US200407578-A1.
XX
XX 22-APR-2004.
XX
XX 02-SEP-2003; 2003US-00653528.
XX
XX 14-JUN-2002; 2002US-00173192.
XX
XX (MONI/) MONIA B P.
XX PA (DOBI/) DOBIE K W.
XX
XX Monia BP, Dobie KM;
XX
XX WPI, 2004-340037/31.
XX
XX New compound, having a sequence targeted to a coding region of a nucleic
XX acid encoding human histone deacetylase 2, useful for preparing a
XX composition for treating hyperproliferative disorders, e.g., cancer.
XX
XX Example 15; SEQ ID NO 32; 47pp; English.
XX
XX The invention relates to antisense compounds, compositions and methods
XX for modulating the expression of histone deacetylase 2 (HDAC2). HDAC2 is
XX also known as HDAC-2, hdac2, human RPD3 and hRPD3. The composition
XX comprises antisense compounds that can be targeted towards HDAC2. The
XX compound is useful for preparing a composition for treating

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OM nucleic - nucleic search, using sw model

Run on: March 1, 2006, 22:25:00 ; Search time 336.667 Seconds
(without alignments)
395.922 Million cell updates/sec

Title: US-10-653-528-32

Perfect score: 20
Sequence: 1 ataaaagcttcacac 20

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 333346308 residues

Total number of hits satisfying chosen parameters: 5180220

Minimum DB seq length: 0
Maximum DB seq length: 80

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

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8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*
14: geneseqn2005s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	20	12	ADJ27015 Human his
2	20	100.0	20	12	ADN49061 Human HDA
3	17.4	87.0	19	14	ADZ78744 N-Ras sIR
4	17.4	87.0	19	14	ADZ78853 N-Ras sIR
5	17	85.0	20	12	ADJ27026 Human his
6	17	85.0	20	12	ADJ27050 Human his
7	17	85.0	20	12	ADN49096 Human his
8	17	85.0	20	12	ADN49072 Human HDA
9	16.4	82.0	45	14	AEA02875 Bacillus
10	16.4	82.0	45	14	AEA02869 Bacillus
11	16.4	82.0	45	14	AEA02849 Bacillus
12	16.4	82.0	45	14	AEA02855 Bacillus
13	15.8	79.0	33	12	ADK67815 Francisel
14	15.4	77.0	18	3	AAA07003 Human Sma
15	15.2	76.0	33	5	AAA09127 Neisseria
16	15.2	76.0	33	5	AA543911 Neisseria
17	15.2	76.0	60	13	AD553635 Eucalyptu
18	14.8	74.0	25	9	ACK18857 Human mlc
19	14.8	74.0	25	9	ACK18856 Human mlc

20	14.8	74.0	33	6	AAL51793 Histone a
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23	14.4	72.0	22	9	ACF05858 Hamster I
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26	14.4	72.0	30	6	AB555383 Arabidops
27	14.4	72.0	33	12	ADU66058 Primer 11
28	14.4	72.0	42	8	AD528229 Human Mow
29	14.4	72.0	44	6	AB555373 Arabidops
30	14.4	72.0	45	2	AAT58883 Monospeci
31	14.4	72.0	51	4	AAL28073 Human SNP
32	14.4	72.0	61	14	AD297451 SNP conta
33	14.2	71.0	23	10	ADC98425 LUM 01 po
34	14.2	71.0	29	4	AAF58627 Murine N-
35	14.2	71.0	42	4	AAF57051 P. furios
36	14.2	71.0	48	4	AAF29302 Primer ba
37	14.2	71.0	48	4	AAF29318 Primer ba
38	14.2	71.0	48	4	AAF29294 Primer ba
39	14.2	71.0	48	4	AAF29313 Primer ba
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41	14.2	71.0	60	6	ABN41091 Human gpl
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46	14	70.0	33	10	ADK82566 Human res
47	14	70.0	34	4	AAH7361 L-lactic
48	14	70.0	34	6	ABL40059 DNA-cyste
49	14	70.0	34	6	ABA96937 UGT and c
50	14	70.0	34	6	AA147091 Human reg
51	14	70.0	34	6	AB221329 Human pro
52	14	70.0	34	6	ABV99614 Methlonin
53	14	70.0	34	6	ABV76425 S24e moti
54	14	70.0	34	6	ABV76569 Human mat
55	14	70.0	34	6	ABA92917 Human g1y
56	14	70.0	34	6	ABA96885 Retinal b
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58	14	70.0	34	6	ABO79332 Human pro
59	14	70.0	34	6	ABO78884 Human res
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79	14	70.0	34	6	AB221343 Nltrogen
80	14	70.0	34	6	AAL51179 Bioplectin
81	14	70.0	34	6	AB270343 Beta_lact
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84	14	70.0	34	6	AB155515 Human rib
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91	14	70.0	34	6	ABK90422 Human pro
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[illegible]

SOURCE	Unknown.
ORGANISM	Unclassified.
REFERENCE	1 (bases 1 to 27)
AUTHORS	Adams,C.W., Carter,P.J., Fendly,B.M. and Gurney,A.L.
TITLE	Agonist antibodies
JOURNAL	Patent: US 6342220-A 17 29-JAN-2002;
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Best Local Similarity	80.0%; Pred. No. 3.6e+05;
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Db	24 ATCAAGCATCTCACCAC 5
RESULT 28	
ARS40638/C	ARS40638 27 bp DNA linear PAT 08-OCT-2004
LOCUS	Sequence 17 from patent US 6737249.
DEFINITION	ARS40638
ACCESSION	ARS40638
VERSION	ARS40638.1 GI:53931919
KEYWORDS	.
SOURCE	Unknown.
ORGANISM	Unclassified.
REFERENCE	1 (bases 1 to 27)
AUTHORS	Adams,C.W., Carter,P.J., Fendly,B.M. and Gurney,A.L.
TITLE	Agonist antibodies
JOURNAL	Patent: US 6737249-A 17 18-MAY-2004;
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Best Local Similarity	80.0%; Pred. No. 3.6e+05;
Matches	16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY	1 ATAAAGCTTCTTCACAC 20
Db	24 ATCAAGCATCTCACCAC 5
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ARS80714	ARS80714 27 bp DNA linear PAT 15-DEC-2004
LOCUS	Sequence 10 from patent US 6790444.
DEFINITION	ARS80714
ACCESSION	ARS80714
VERSION	ARS80714.1 GI:56611224
KEYWORDS	.
SOURCE	Unknown.
ORGANISM	Unclassified.
REFERENCE	1 (bases 1 to 27)
AUTHORS	Le,J., Vilcek,J., Daddona,P., Ghrayeb,J., Knight,D. and Siegel,S.
TITLE	Anti-TNF antibodies and peptides of human necrosis factor
JOURNAL	Patent: US 6790444-A 10 14-SEP-2004;
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ORIGIN	

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ACCESSION COS37841
VERSION COS37841.1 GI:41504105
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.

REFERENCE
AUTHORS Shoshan,A., Wasserman,A., Mintz,E., Mintz,L. and Faigler,S.
TITLE Oligonucleotide library for detecting rna transcripts and splice
variants that populate a transcriptome
JOURNAL Patent: WO 0210449-A 7476 07-FEB-2002;
CompuGen Inc. (US)
FEATURES
source 1..60
/organism="Homo sapiens"
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Best Local Similarity 88.2%; Pred. No.2.6e+05;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 AAAAAGCTTCTTCAACA 19
Db 57 AACAACTTCTTCTACA 41

RESULT 22
LOCUS AX485897/c 65 bp DNA linear PAT 16-AUG-2002
DEFINITION Sequence 3197 from Patent WO02053728.
ACCESSION AX485897
VERSION AX485897.1 GI:22320113
KEYWORDS
SOURCE Candida albicans
ORGANISM Candida albicans
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; mitosporic Saccharomycetales; Candida.

REFERENCE
AUTHORS Roemer,T., Jiang,B., Boone,C., Bussey,H. and Ohlsen,K.L.
TITLE Gene disruption methodologies for drug target discovery
JOURNAL Patent: WO 02053728-A 3197 11-JUL-2002;
Elicira Pharmaceuticals, Inc. (US)
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/mol_type="unassigned DNA"
/db_xref="taxon:5476"

ORIGIN
Query Match 69.0%; Score 13.8; DB 6; Length 65;
Best Local Similarity 88.2%; Pred. No.2.5e+05;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TAAAAAGCTTCTTCAAC 18
Db 33 TAAAAAGCTTCTTAAAC 17

RESULT 23
LOCUS AX494015/c 24 bp DNA linear PAT 26-SEP-2002
DEFINITION Sequence 989 from Patent WO02059355.
ACCESSION AX494015

VERSION AX494015.1 GI:23339647
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.

REFERENCE
AUTHORS Fieldhouse,D. and Koblir,D.
TITLE Polynucleotides for use as tags and tag complements, manufacture
and use thereof
JOURNAL Patent: WO 02059355-A 989 01-AUG-2002;
TM BIOSCIENCE CORP (CA)
FEATURES
source 1..24
Location/Qualifiers
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/db_xref="taxon:32630"
/note="Artificially Synthesized DNA Sequence"

ORIGIN
Query Match 68.0%; Score 13.6; DB 6; Length 24;
Best Local Similarity 80.0%; Pred. No.3.7e+05;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 ATAAAAAGCTTCTTCAAC 20
Db 23 ATAAACATCTTTATCAAC 4

RESULT 24
LOCUS BD080955/c 27 bp DNA linear PAT 27-AUG-2002
DEFINITION Agonist antibodies against thrombopoietin receptor and therapeutic
use thereof.
ACCESSION BD080955
VERSION BD080955.1 GI:22626558
KEYWORDS JP 2001513999-A/9.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
1 (bases 1 to 27)
REFERENCE Adams,C.W., Carter,P.J., Fendly,B.M. and Gurney,A.L.
AUTHORS Agonist antibodies against thrombopoietin receptor and therapeutic
TITLE use thereof
JOURNAL Patent: JP 2001513999-A 9 11-SEP-2001;
GENENTECH INC
COMMENT OS Homo sapiens (human)
PN JP 2001513999-A/9
PD 11-SEP-2001
PF 21-AUG-1998 JP 2000507802
PR 25-AUG-1997 US 08/918148
PT CAMELIDIA W ADAMS,PAUL J CARTER,BRIAN M FENDLY,AUSTIN L GURNEY
PC C12N15/09,A61K31/711,A61K39/395,A61P7/00,A61P7/04,A61P7/06, PC
A61P37/02,
PC C07K16/28,C07K17/00,C07K19/00,C12N5/10,C12P21/08,C12N15/00, PC
C12N5/00
CC Agonist antibodies against thrombopoietin receptor and CC
therapeutic use
CC Key Location/Qualifiers
FT source 1..27
FT Location/Qualifiers
1..27
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match 68.0%; Score 13.6; DB 6; Length 27;
Best Local Similarity 80.0%; Pred. No.3.6e+05;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

TITLE	Masuko, Y.				
JOURNAL	Full-length cDNAs Patent: EP 1293569-A 3375 19-MAR-2003; Helix Research Institute (JP) ; Research Association for Biotechnology (JP) Location/Qualifiers				
FEATURES	1..20 /organism="synthetic construct" /mol_type="unassigned DNA" /db_xref="taxon:32630" /note="an artificially synthesized primer sequence"				
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Query Match	69.0%;	Score 13.8;	DB 6;	Length 20;	
Best Local Similarity	88.2%;	Pred. No. 3.1e+05;			
Matches	15;	Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0;
Oy	4	AAAGCTTCTCAACAC	20		
Db	1	AACAGCTTCTCATCAC	17		
RESULT 18					
AX494024/c	24 bp	DNA	linear	PAT 26-SEP-2002	
LOCUS					
DEFINITION	Sequence 998 from Patent WO02059355.				
ACCESSION	AX494024				
VERSION	AX494024.1 GI:23339656				
KEYWORDS					
SOURCE	synthetic construct				
ORGANISM	synthetic construct				
REFERENCE	other sequences; artificial sequences.				
AUTHORS	1				
TITLE	Fieldhouse, D. and Kobler, D.				
JOURNAL	Polynucleotides for use as tags and tag complements, manufacture and use thereof Patent: WO 02059355-A 998 01-AUG-2002; TM BIOSCIENCE CORP (CA) Location/Qualifiers				
FEATURES	1..24 /organism="synthetic construct" /mol_type="unassigned DNA" /db_xref="taxon:32630" /note="Artificially Synthesized DNA Sequence"				
ORIGIN					
Query Match	69.0%;	Score 13.8;	DB 6;	Length 24;	
Best Local Similarity	88.2%;	Pred. No. 3e+05;			
Matches	15;	Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0;
Oy	1	ATAAAGCTTCTTCAA	17		
Db	17	ATAACAATCTTCTCAA	1		
RESULT 19					
CO863125/c	25 bp	DNA	linear	PAT 10-SEP-2004	
LOCUS					
DEFINITION	Sequence 1758 from Patent WO2004072265.				
ACCESSION	CO863125				
VERSION	CO863125.1 GI:51984114				
KEYWORDS					
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominiidae; Homo.				
AUTHORS	1				
TITLE	Burczynski, M., Twine, N., Dörner, A. J. and Trepicchio, W. L.				
JOURNAL	METHODS FOR MONITORING DRUG ACTIVITIES IN VIVO /I Patent: WO 2004072265-A 1758 26-AUG-2004; Wyeth (US); Burczynski, Michael E. (US); Twine, Natalie C. (US); Dörner, Andrew J. (US); Trepicchio, William L. (US)				

FEATURES	Location/Qualifiers
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ORIGIN	
Query Match	69.0%; Score 13.8; DB 6; Length 25;
Best Local Similarity	88.2%; Pred. No. 3e+05;
Matches 15; Conservative	0; Mismatches 2; Indels 0; Gaps 0;
QY	4 AAAAGCTTCTTCAAC 20 25 AAACCTTCTTCAAC 9
RESULT 20	
ATH523045	55 bp DNA linear PLN 29-MAR-2003
LOCUS	
DEFINITION	Arabidopsis thaliana T-DNA flanking sequence, left border, clone 305B04.
ACCESSION	AJ523045
VERSION	AJ523045.1 GI:26791281
KEYWORDS	left border; T-DNA flanking sequence.
SOURCE	Arabidopsis thaliana (thale cress)
ORGANISM	Arabidopsis thaliana Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE	1 Brunaud V., Balergue S., Dubreucq B., Aubourg S., Samson F., Chauvin S., Bechtold N., Craud C., Dehose R., Pelletier G., Lepointec L., Caboche M., and Lecharny A. T-DNA integration into the Arabidopsis genome depends on sequences of pre-insertion sites EMBO Rep. 3 (12), 1152-1157 (2002)
AUTHORS	2 (bases 1 to 55) Balergue S. Direct Submission Submitted (21-NOV-2002) Balergue S., UMRGV, INRA/CNRS, 2 rue Gaetan Cremieux, 91057 Evry cedex, FRANCE
JOURNAL	PCR was performed on DNA from transformants of Arabidopsis thaliana plants from INRA (Versailles). The DNA fragment(s) resulting from the PCR were directly sequenced from the left or the right border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at http://dbsgap.versailles.inra.fr/publiclines/. This sequence has been generated in the framework of the French plant genomes program 'Genoplante' (http://www.genoplante.com and http://genoplante-info.inbioigen.fr).
COMMENT	Location/Qualifiers 1..55 /organism="Arabidopsis thaliana" /mol_type="genomic DNA" /db_xref="taxon:3702" /clone="305B04" /clone_jlb="Arabidopsis thaliana T-DNA insertion lines" /ecotype="wasstlewskija" 1..55 /note="T-DNA flanking sequence left border"
FEATURES	
source	
misc_feature	
ORIGIN	
QY	2 TAAAAGCTTCTTCAAC 18 5 TAAAACCTTCTTCAAC 21
DB	

RESULT 13	AX077820	29 bp	DNA	linear	PAT 22-FEB-2001
LOCUS	AX077820				
DEFINITION	Sequence 21 from Patent WO0107627.				
ACCESSION	AX077820				
VERSION	AX077820.1	GI:13157676			
KEYWORDS					
SOURCE					
ORGANISM	synthetic construct				
	synthetic construct				
	other sequences; artificial sequences.				
REFERENCE	1				
AUTHORS	Eisen, A.				
TITLE	Drosophila recombination-associated protein and methods for use				
JOURNAL	Patent: WO 0107627-A 21 01-FEB-2001;				
	ALBERT EINSTEIN COLLEGE OF MEDICINE OF YESHIVA UNIVERSITY (US)				
FEATURES					
source					
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	/organism="synthetic construct"				
	/mol_type="unassigned DNA"				
	/db_xref="taxon:32630"				
	/note="Oligonucleotide"				
ORIGIN					

	Query Match	71.0%;	Score 14.2;	DB 6;	Length 29;
	Best Local Similarity	84.2%;	Pred. No. 1.9e+05;		
Matches	16; Conservative	0;	Mismatches	3;	Indels 0;
OY	2 TAAAAAGCTTCTCAACAC	20			
Db	6 TAAAAAGCTTATTCAGCAC	24			
RESULT 14					
LOCUS	AX081663		42 bp	DNA	linear PAT 27-FEB-2001
DEFINITION	Sequence 12 from Patent WO0109347.				
ACCESSION	AX081663				
VERSION	AX081663.1 GI:13170487				
KEYWORDS					
SOURCE					
ORGANISM	synthetic construct				
REFERENCE	synthetic construct				
AUTHORS	other sequences; artificial sequences.				
TITLE	1 Hoegrefe H.H., Cline J.M., Hansen C.J. and Borns M.C.				
JOURNAL	Archaeal replication accessory factors and methods of use				
	Patent: WO 0109347-A 12 08-FEB-2001;				
	STRATEGEM (US)				
FEATURES					
source	Location/Qualifiers				
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	/note="Primer"				
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	Query Match	71.0%;	Score 14.2;	DB 6;	Length 42;
	Best Local Similarity	84.2%;	Pred. No. 1.8e+05;		
Matches	16; Conservative	0;	Mismatches	3;	Indels 0;
OY	1 ATAAAAAGCTTCTCAACA	19			
Db	19 ATAAAGGCTTCATPAACA	37			
RESULT 15					
LOCUS	AR583303		47 bp	DNA	linear PAT 15-DEC-2004
DEFINITION	Sequence 1230 from patent US 6794143.				
ACCESSION	AR583303				
VERSION	AR583303.1 GI:56619644				
KEYWORDS					

SOURCE	Unknown.
ORGANISM	Unknown.
REFERENCE	Unclassified.
AUTHORS	1 (bases 1 to 47)
TITLE	Blumentfeld,M., Bougueleret,L., Chumakov,I. and Cohen,A.
JOURNAL	Ballester markers derived from genomic regions carrying genes involved in arachidonic acid metabolism
	Patent: US 6794143-A 1230 21-SEP-2004;
	Genet S.A.;;
PRX;	
FEATURES	
source	Location/Qualifiers
	1..47
	/organism="unknown"
	/mol_type="genomic DNA"
ORIGIN	
Query Match	71.0%; Score 14.2; DB 6; Length 47;
Best Local Similarity	84.2%; Pred. No. 1.7e+05;
Matches	16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY	1 ATAAAAGCTTCTCACA 19
Db	25 ATAAAAAATCTTTAACA 7

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[illegible][illegible]

RESULT 5	BD175003	29 bp	DNA	linear	PAT 18-MAR-2003
LOCUS	BD175003	Cis-regulatory sequence exhibiting performance of regulating the expression of DNA damage-responsive gene of higher plants.			
DEFINITION	BD175003				
ACCESSION	BD175003.1	GI:29120697			
VERSION	JP 2002272469-A/16.				
KEYWORDS	JP 2002272469-A/16.				
SOURCE	synthetic construct				
ORGANISM	other sequences; artificial sequences.				
REFERENCE	1 (bases 1 to 29)				
AUTHORS	Hiratsuka, K., Takase, N. and Maeda, T.				
TITLE	Cis-regulatory sequence exhibiting performance of regulating the expression of DNA damage-responsive gene of higher plants				
JOURNAL	Patent: JP 2002272469-A 16 24-SEP-2002;				
COMMENT	PRESIDENT OF NARA INSTITUTE OF SCIENCE AND TECHNOLOGY				
	OS Artificial Sequence				
	PN JP 2002272469-A/16				
	PD 24-SEP-2002				
	PF 19-MAR-2001	JP 2001079524			
	PI KAZUOKI HIRATSUKA, NAOFUMI TAKASE, TOMOHIDE MAEDA	PC			
	C12N15/09, A01H5/00, C12N5/10, C12N15/00, C12N5/00 CC	Artificial			
	sequence: primer sequence				
	FH Key	location/Qualifiers			
	FT source	1..29	/organism='Artificial Sequence'.		
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		1..29	/organism="synthetic construct"		
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ORIGIN					
Query Match	72.0%;	Score 14.4;	DB 6;	Length 29;	
Best Local Similarity	93.8%;	Pred. No. 1.5e+05;			
Matches	15; Conservative	0;	Mismatches	1;	Indels 0; Gaps 0;
QY	4 AAAAGCTTCTTCACA	19			
DB	7 AAAAGCTTCTTCACA	22			
RESULT 6	BD174998/c	30 bp	DNA	linear	PAT 18-MAR-2003
LOCUS	BD174998	Cis-regulatory sequence exhibiting performance of regulating the expression of DNA damage-responsive gene of higher plants.			
DEFINITION	BD174998				
ACCESSION	BD174998.1	GI:29120692			
VERSION	JP 2002272469-A/11.				
KEYWORDS	JP 2002272469-A/11.				
SOURCE	synthetic construct				
ORGANISM	synthetic construct				
REFERENCE	1 (bases 1 to 30)				
AUTHORS	Hiratsuka, K., Takase, N. and Maeda, T.				
TITLE	Cis-regulatory sequence exhibiting performance of regulating the expression of DNA damage-responsive gene of higher plants				
JOURNAL	Patent: JP 2002272469-A 11 24-SEP-2002;				
COMMENT	PRESIDENT OF NARA INSTITUTE OF SCIENCE AND TECHNOLOGY				
	OS Artificial Sequence				
	PN JP 2002272469-A/11				
	PD 24-SEP-2002				
	PF 19-MAR-2001	JP 2001079524			
	PI KAZUOKI HIRATSUKA, NAOFUMI TAKASE, TOMOHIDE MAEDA	PC			
	C12N15/09, A01H5/00, C12N5/10, C12N15/00, C12N5/00 CC	Artificial			
	sequence: primer sequence				
	FH Key	location/Qualifiers			
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FEATURES	source	location/Qualifiers			
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			/mol_type="genomic DNA"		
			/db_xref="taxon:32630"		

ORIGIN	/organism="synthetic construct" /mol_type="genomic DNA" /db_xref="taxon:32630"			
Query Match	72.0%;	Score 14.4;	DB 6;	Length 30;
Best Local Similarity	93.8%;	Pred. No. 1.5e+05;		
Matches 15;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0
QY	4 AAAAGCTTCTTCACCA 19 			
Db	29 AAAGCTTCTTCACCA 14 			
RESULT 7	AA664096/c 42 bp DNA linear PAT 22-MAR-2003			
LOCUS	AX664096			
DEFINITION	Sequence 31 from Patent WO02092624.			
ACCESSION	AX664096			
VERSION	AX664096.1 GI:29164108			
KEYWORDS	synthetic construct			
SOURCE	synthetic construct			
ORGANISM	other sequences; artificial sequences.			
REFERENCE	1			
AUTHORS	Carlton,M., Aparicio,S., Dixon,J., Thresher,R. and Zahn,D.			
TITLE	Receptor			
JOURNAL	Patent: WO 02092624-A 31 21-NOV-2002;			
FEATURES	Paradigm Therapeutics Limited (GB)			
source	location/Qualifiers			
	1..42			
	/organism="synthetic construct"			
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	/db_xref="taxon:32630"			
	/note="Primer"			
ORIGIN				
Query Match	72.0%;	Score 14.4;	DB 6;	Length 42;
Best Local Similarity	93.8%;	Pred. No. 1.4e+05;		
Matches 15;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;
QY	1 ATAAAGCTTCTTCA 16 			
Db	41 ATAAAGCTTCTTCA 26 			
RESULT 8	BD174988/c 44 bp DNA linear PAT 18-MAR-2003			
LOCUS	BD174988			
DEFINITION	Cis-regulatory sequence exhibiting performance of regulating the expression of DNA damage-responsive gene of higher plants.			
ACCESSION	BD174988			
VERSION	BD174988.1 GI:29120682			
KEYWORDS	JP 2002272469-A/1.			
SOURCE	Arabidopsis thaliana (thale cress)			
ORGANISM	Arabidopsis thaliana			
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.			
	1 (bases 1 to 44)			
	Hiratsuka,K., Takase,N. and Maeda,T.			
REFERENCE	Cis-regulatory sequence exhibiting performance of regulating the expression of DNA damage-responsive gene of higher plants			
AUTHORS	Patent: JP 2002272469-A 1 24-SEP-2002;			
TITLE	PRESIDENT OF NARA INSTITUTE OF SCIENCE AND TECHNOLOGY			
JOURNAL	OS Arabidopsis thaliana (thale cress)			
COMMENT	PN JP 2002272469-A/1			
	PD 24-SEP-2002			
	PF 19-MAR-2001 JP 2001079524			
	PI KAZUYUKI HIRATSUKA, NAOFUMI TAKASE, TOMOHIDE MAEDA PC			
	CI2N15/09,A01H5/00,CI2N5/10,CI2N15/00,CI2N5/00 CC Cis-regulatory			
	sequence exhibiting performance of regulating CC			
	expression			

C 92 12.8 64.0 26 6 AR431408 Sequence
 C 93 12.8 64.0 27 6 BD068485 Enzymatic
 C 94 12.8 64.0 27 6 BD068712 Enzymatic
 C 95 12.8 64.0 27 6 AR184640 Sequence
 C 96 12.8 64.0 27 6 AR190864 Sequence
 C 97 12.8 64.0 27 6 AR402985 Sequence
 C 98 12.8 64.0 27 6 AR403212 Sequence
 C 99 12.8 64.0 32 6 BD166376 DNA encod
 100 12.8 64.0 32 6 BD166383

ALIGNMENTS

RESULT 1
 CS136517/c CS136517 19 bp RNA linear PAT 09-AUG-2005
 LOCUS Sequence 254 from Patent WO2005040379.
 ACCESSION CS136517
 VERSION CS136517.1 GI:72062098
 KEYWORDS
 SOURCE
 ORGANISM
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL

Mcswigen, J.
 RNA interference mediated inhibition of RAS gene expression using
 short interfering Nucleic Acid (siNA)
 Patent: WO 2005040379-A 254 06-MAY-2005;
 Sirta Therapeutics, Inc. (US)
 Location/Qualifiers

FEATURES
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 /organism="synthetic construct"
 /mol_type="unassigned RNA"
 /db_xref="taxon:32630"
 /note="Synthetic"

ORIGIN

Query Match 87.0%; Score 17.4; DB 6; Length 19;
 Best Local Similarity 94.7%; Pred. No. 6.9e+03;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 2 TAAAGCTTCTCAAC 20
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 Db 19 TAAAGCATCTCAAC 1

RESULT 2
 CS136626 CS136626 19 bp RNA linear PAT 09-AUG-2005
 LOCUS Sequence 363 from Patent WO2005040379.
 ACCESSION CS136626
 VERSION CS136626.1 GI:72062239
 KEYWORDS
 SOURCE
 ORGANISM
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL

Mcswigen, J.
 RNA interference mediated inhibition of RAS gene expression using
 short interfering Nucleic Acid (siNA)
 Patent: WO 2005040379-A 363 06-MAY-2005;
 Sirta Therapeutics, Inc. (US)
 Location/Qualifiers

FEATURES
 source
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 /organism="synthetic construct"
 /mol_type="unassigned RNA"
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 /note="Synthetic"

ORIGIN

Query Match 87.0%; Score 17.4; DB 6; Length 19;
 Best Local Similarity 94.7%; Pred. No. 6.9e+03;

Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 2 TAAAGCTTCTCAAC 20
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 Db 1 TAAAGCATCTCAAC 19

RESULT 3
 CQ775506 CQ775506 33 bp DNA linear PAT 06-MAR-2004
 LOCUS Sequence 31 from Patent WO2004013357.
 ACCESSION CQ775506
 VERSION CQ775506.1 GI:45238314
 KEYWORDS
 SOURCE
 ORGANISM

Francisella tularensis
 Francisella tularensis
 Bacteria; Proteobacteria; Gammaproteobacteria; Rhizobiales;
 Francisellaceae; Francisella.

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 McCready, P.M., Radnedge, L., Andersen, G.L., Ott, L.L., Slezak, T.R.,
 Kuczmarski, T.A. and Vitalis, E.A.
 Nucleotide sequences specific to Francisella tularensis and methods
 for the detection of Francisella tularensis
 Patent: WO 2004013357-A 31 12-FEB-2004;
 The Regent of the University of California (US)
 Location/Qualifiers

FEATURES
 source
 1..33
 /organism="Francisella tularensis"
 /mol_type="unassigned DNA"
 /db_xref="taxon:263"

ORIGIN

Query Match 79.0%; Score 15.8; DB 6; Length 33;
 Best Local Similarity 89.5%; Pred. No. 3.4e+04;
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 ATAAAGCTTCTCAACA 19
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 Db 13 ATCAAGAGCTTCTCAACA 31

RESULT 4
 AX236476 AX236476 33 bp DNA linear PAT 26-SEP-2001
 LOCUS Sequence 169 from Patent WO0164922.
 ACCESSION AX236476
 VERSION AX236476.1 GI:15796062
 KEYWORDS
 SOURCE
 ORGANISM

synthetic construct
 other sequences; artificial sequences.
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 Heterologous expression of neisserial proteins
 Patent: WO 0164922-A 169 07-SEP-2001;
 Chiron Spa (IT)
 Location/Qualifiers

FEATURES
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 /organism="synthetic construct"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32630"
 /note="Oligonucleotide"

ORIGIN

Query Match 76.0%; Score 15.2; DB 6; Length 33;
 Best Local Similarity 85.0%; Pred. No. 6.4e+04;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 1 ATAAAGCTTCTCAAC 20
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 Db 13 ATGAAGCTTCTCAAAC 32

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: March 1, 2006, 22:25:24 ; Search time 589.333 Seconds
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Title: US-10-653-528-32
Perfect score: 20
Sequence: 1 ataaaagctctcaacac 20

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues
Total number of hits satisfying chosen parameters: 2389942

Minimum DB seq length: 0
Maximum DB seq length: 80

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

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1: gb_pa:*
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6: gb_pat:*
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8: gb_pr:*
9: gb_ro:*
10: gb_sts:*
11: gb_gy:*
12: gb_un:*
13: gb_vl:*
14: gb_hcg:*
15: gb_pl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	17.4	87.0	19	6	CS136626	Sequence
3	15.8	79.0	33	6	C0775506	Sequence
4	15.2	76.0	33	6	AX236476	Sequence
5	14.4	72.0	29	6	BD175003	Cis-regul
6	14.4	72.0	30	6	BD174998	Cis-regul
7	14.4	72.0	42	6	AX664096	Sequence
8	14.4	72.0	44	6	BD174988	Cis-regul
9	14.4	72.0	45	6	AR243936	Sequence
10	14.4	72.0	51	6	CQ002641	Sequence
11	14.2	71.0	29	6	AR615715	Sequence
12	14.2	71.0	29	6	AR641140	Sequence
13	14.2	71.0	29	6	AX077820	Sequence
14	14.2	71.0	42	6	AX081663	Sequence
15	14.2	71.0	47	6	AR583303	Sequence
16	14.2	71.0	60	6	CQ544204	Sequence
17	13.8	69.0	20	6	AX716691	Sequence
18	13.8	69.0	24	6	AX494024	Sequence

C	19	13.8	69.0	25	6	CQ863125	CQ863125 Sequence
C	20	13.8	69.0	55	15	ATMS23045	AJ523045 Arabidops
C	21	13.8	69.0	60	6	CQ537841	CQ537841 Sequence
C	22	13.8	69.0	65	6	AX485897	AX485897 Sequence
C	23	13.6	68.0	24	6	AX494015	AX494015 Sequence
C	24	13.6	68.0	27	6	BD080955	BD080955 Agoniat a
C	25	13.6	68.0	27	6	160229	160229 Sequence 10
C	26	13.6	68.0	27	6	185503	185503 Sequence 10
C	27	13.6	68.0	27	6	AR183482	AR183482 Sequence
C	28	13.6	68.0	27	6	AR540638	AR540638 Sequence
C	29	13.6	68.0	27	6	AR580714	AR580714 Sequence
C	30	13.6	68.0	27	6	AR629087	AR629087 Sequence
C	31	13.6	68.0	35	15	ATMS30867	AJ530867 Arabidops
C	32	13.6	68.0	50	6	AX190233	AX190233 Sequence
C	33	13.6	68.0	78	10	BX323292	BX323292 Arabidops
C	34	13.4	67.0	19	6	CS096246	CS096246 Sequence
C	35	13.4	67.0	19	6	CS096345	CS096345 Sequence
C	36	13.4	67.0	30	6	BD175007	BD175007 Cis-regul
C	37	13.4	67.0	30	6	AX665214	AX665214 Sequence
C	38	13.4	67.0	40	6	AR486948	AR486948 Sequence
C	39	13.4	67.0	40	6	AR654759	AR654759 Sequence
C	40	13.4	67.0	40	6	AX418568	AX418568 Sequence
C	41	13.4	67.0	40	6	AX952307	AX952307 Sequence
C	42	13.4	67.0	41	6	AX516872	AX516872 Sequence
C	43	13.4	67.0	41	6	AX519382	AX519382 Sequence
C	44	13.4	67.0	24	6	AR001225	AR001225 Sequence
C	45	13.2	66.0	24	6	AR008248	AR008248 Sequence
C	46	13.2	66.0	24	6	AR010175	AR010175 Sequence
C	47	13.2	66.0	24	6	AR064099	AR064099 Sequence
C	48	13.2	66.0	24	6	I38288	I38288 Sequence 3
C	49	13.2	66.0	24	6	I4831	I4831 Sequence 9
C	50	13.2	66.0	30	6	CQ856917	CQ856917 Sequence
C	51	13.2	66.0	30	6	AX790859	AX790859 Sequence
C	52	13.2	66.0	30	6	AX792031	AX792031 Sequence
C	53	13.2	66.0	37	6	I42715	I42715 Sequence 11
C	54	13.2	66.0	44	6	AR038929	AR038929 Sequence
C	55	13.2	66.0	44	6	AR091295	AR091295 Sequence
C	56	13.2	66.0	44	6	AR123420	AR123420 Sequence
C	57	13.2	66.0	46	6	AR564987	AR564987 Sequence
C	58	13.2	66.0	46	6	AR137670	AR137670 Sequence
C	59	13.2	66.0	51	6	AX117581	AX117581 Sequence
C	60	13.2	66.0	54	6	AR121386	AR121386 Sequence
C	61	13.2	66.0	54	6	AR124118	AR124118 Sequence
C	62	13.2	66.0	54	6	E36141	E36141 Chimeric se
C	63	13.2	66.0	54	6	AR437559	AR437559 Sequence
C	64	13.2	66.0	54	6	AX022600	AX022600 Sequence
C	65	13.2	66.0	57	6	BD190359	BD190359 Propylac
C	66	13.2	66.0	60	2	AY059239S7	AY059245 Cario ca
C	67	13.2	66.0	60	6	CQ546395	CQ546395 Sequence
C	68	13.2	66.0	65	6	CQ532663	CQ532663 Sequence
C	69	13.2	66.0	65	6	CQ559050	CQ559050 Sequence
C	70	13.2	66.0	66	6	AX022876	AX022876 Sequence
C	71	13.2	66.0	73	6	AR356290	AR356290 Sequence
C	72	13.2	66.0	73	6	AR537846	AR537846 Sequence
C	73	13.2	66.0	73	6	AX516707	AX516707 Sequence
C	74	13.2	66.0	41	6	AX518871	AX518871 Sequence
C	75	13.2	66.0	41	6	CQ553170	CQ553170 Sequence
C	76	13.2	66.0	17	6	BD257497	BD257497 Regulatio
C	77	12.8	64.0	17	6	BD257498	BD257498 Regulatio
C	78	12.8	64.0	17	6	AX216507	AX216507 Sequence
C	79	12.8	64.0	18	6	AX149015	AX149015 Sequence
C	80	12.8	64.0	20	6	AX149014	AX149014 Sequence
C	81	12.8	64.0	20	6	AX149016	AX149016 Sequence
C	82	12.8	64.0	22	6	CQ778574	CQ778574 Sequence
C	83	12.8	64.0	22	6	CQ807388	CQ807388 Sequence
C	84	12.8	64.0	22	6	CS124771	CS124771 Sequence
C	85	12.8	64.0	22	6	AX796012	AX796012 Sequence
C	86	12.8	64.0	22	6	AX8252540	AX8252540 Sequence
C	87	12.8	64.0	22	6	AX825619	AX825619 Sequence
C	88	12.8	64.0	22	6	AX826180	AX826180 Sequence
C	89	12.8	64.0	25	6	CQ945846	CQ945846 Sequence
C	90	12.8	64.0	26	6	AR099874	AR099874 Sequence
C	91	12.8	64.0	26	6		

US-11-054-047-69

Search completed: March 2, 2006, 01:39:37
Job time : 498.333 secs

Query Match 67.0%; Score 13.4; DB 12; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.5e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 ATATTATGGAATGA 20
DB 19 ATATTATGGAATGA 5

RESULT 29

US-11-054-047-197
; Sequence 197, Application US/11054047
; Publication No. US20050287128A1
; GENERAL INFORMATION:
; APPLICANT: Sirta Therapeutics, Inc.
; APPLICANT: Guericiolini, Roberto
; APPLICANT: Robin, Howard
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of TGF-Beta and TGF-Beta
; TITLE OF INVENTION: Receptor Gene Expression Using Short Interfering Nucleic Acid
; TITLE OF INVENTION: (siRNA)
; FILE REFERENCE: 400/248 (MHB02-1193-E)
; CURRENT APPLICATION NUMBER: US/11/054,047
; CURRENT FILING DATE: 2005-02-09
; NUMBER OF SEQ ID NOS: 855
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 197
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-11-054-047-197

Query Match 67.0%; Score 13.4; DB 12; Length 19;
Best Local Similarity 53.3%; Pred. No. 1.5e+03;
Matches 8; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 6 ATATTATGGAATGA 20
DB 1 AUUUUUGAUAUCA 15

RESULT 30

US-10-310-914A-1285165/C
; Sequence 1285165, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shlier, Kuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087,0200,CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1285165
; LENGTH: 20
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1285165

Query Match 67.0%; Score 13.4; DB 8; Length 20;
Best Local Similarity 93.3%; Pred. No. 1.5e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCCCATTTATG 15
DB 16 TCTCCATTTATG 2

Db 24 TCAACGTATTATGGAAGA 5

RESULT 24

US-11-121-849-126576
; Sequence 126576, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 126576
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-126576

Query Match 68.0%; Score 13.6; DB 12; Length 25;
Best Local Similarity 80.0%; Pred. No. 1.3e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 TCCCCATATTATGGAATGA 20
Db 2 TCTCCATCTTTATAGAAGA 21

RESULT 25

US-11-121-849-416798/C
; Sequence 416798, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 416798
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-416798

Query Match 68.0%; Score 13.6; DB 12; Length 25;
Best Local Similarity 80.0%; Pred. No. 1.3e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 TCCCCATATTATGGAATGA 20
Db 24 TACACAGATGTATGGAATGA 5

RESULT 26

US-11-175-859-90816
; Sequence 90816, Application US/11175859
; Publication No. US20060024715A1
; GENERAL INFORMATION:
; APPLICANT: Affimetrix, Inc.
; APPLICANT: Liu, Guoying et al.
; TITLE OF INVENTION: Method of Analysis of Human Polymorphism
; FILE REFERENCE: 3690.1

; CURRENT APPLICATION NUMBER: US/11/175,859
; CURRENT FILING DATE: 2005-07-05
; PRIOR APPLICATION NUMBER: US 60/585,352
; PRIOR FILING DATE: 2004-07-02
; NUMBER OF SEQ ID NOS: 116251
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 90816
; LENGTH: 50
; TYPE: DNA
; ORGANISM: homo sapien
US-11-175-859-90816

Query Match 68.0%; Score 13.6; DB 12; Length 50;
Best Local Similarity 80.0%; Pred. No. 1.6e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 TCCCCATATTATGGAATGA 20
Db 28 TACCTATATTATAGCAATGA 47

RESULT 27

US-10-310-914A-1019817/C
; Sequence 1019817, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kiyuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes an
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1019817
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1019817

Query Match 67.0%; Score 13.4; DB 8; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.5e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 CATATTATGGAATG 19
Db 15 CATATTATGAGATG 1

RESULT 28

US-11-054-047-69/C
; Sequence 69, Application US/11054047
; Publication No. US20050287128A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Guercolini, Roberto
; APPLICANT: Robin, Howard
; TITLE OF INVENTION: RNA interference Mediated Inhibition of TGF-Beta and TGF-Beta
; TITLE OF INVENTION: Receptor Gene Expression Using Short Interfering Nucleic Acid
; FILE REFERENCE: 400/248 (MHB02-1193-E)
; CURRENT APPLICATION NUMBER: US/11/054,047
; CURRENT FILING DATE: 2005-02-09
; NUMBER OF SEQ ID NOS: 855
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 69
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic

```
US-11-121-849-216448
; Sequence 216448, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; TITLE OF INVENTION: Microarrays
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 216448
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-216448

Query Match      69.0%; Score 13.8; DB 12; Length 25;
Best Local Similarity 88.2%; Pred. No. 1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 CCCATTTTATGGAATG 19
DB 4 CTCACATTATGGAATG 20

RESULT 20
US-11-136-527-228156/c
; Sequence 228156, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeck
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 228156
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Probe
US-11-136-527-228156

Query Match      69.0%; Score 13.8; DB 12; Length 25;
Best Local Similarity 88.2%; Pred. No. 1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 CCATTTTATGGAATGA 20
DB 20 CCATTTTGTGGAAGA 4

RESULT 21
US-11-175-859-31164
; Sequence 31164, Application US/11175859
; Publication No. US20060024715A1
; GENERAL INFORMATION:
; APPLICANT: Aftymetrix, Inc.
; APPLICANT: Liu, Guoying et al.
; TITLE OF INVENTION: Method of Analysis of Human Polymorphism
; FILE REFERENCE: 3690.1
; CURRENT APPLICATION NUMBER: US/11/175,859
; CURRENT FILING DATE: 2005-07-05
; PRIOR APPLICATION NUMBER: US 60/585,352

PRIOR FILING DATE: 2004-07-02
; NUMBER OF SEQ ID NOS: 116251
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 31164
; LENGTH: 50
; TYPE: DNA
; ORGANISM: homo sapien
US-11-175-859-31164

Query Match      69.0%; Score 13.8; DB 12; Length 50;
Best Local Similarity 78.9%; Pred. No. 1.2e+03;
Matches 15; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 TCCCATTTTATGGAATG 19
DB 9 TCTCTATTTATTTGAATG 27

RESULT 22
US-10-310-914A-16897
; Sequence 16897, Application US/10310914A
; Publication No. US2006003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shilley, Kuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 16897
; LENGTH: 76
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-16897

Query Match      69.0%; Score 13.8; DB 8; Length 76;
Best Local Similarity 52.9%; Pred. No. 1.4e+03;
Matches 9; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY 4 CCATTTTATGGAATGA 20
DB 7 CCUUAUUUAGGAUCCA 23

RESULT 23
US-11-121-849-98438/c
; Sequence 98438, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded
; TITLE OF INVENTION: Microarrays
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 98438
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-98438

Query Match      68.0%; Score 13.6; DB 12; Length 25;
Best Local Similarity 80.0%; Pred. No. 1.3e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 TCCCATTTTATGGAATGA 20
```

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; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1224663
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1224663

Query Match      70.0%; Score 14; DB 11; Length 19;
Best Local Similarity 100.0%; Pred. No. 7.3e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 ATATTATGGAATG 19
DB      17 ATATTATGGAATG 4

RESULT 15
US-10-310-914A-318333/C
; Sequence 318333, Application US/10310914A
; Publication No. US2006003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuza
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 318333
; LENGTH: 24
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-318333

Query Match      70.0%; Score 14; DB 8; Length 24;
Best Local Similarity 100.0%; Pred. No. 7.8e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 TATTATGGAATGA 20
DB      19 TATTATGGAATGA 6

RESULT 16
US-11-175-859-97395
; Sequence 97395, Application US/11175859
; Publication No. US20060024715A1
; GENERAL INFORMATION:
; APPLICANT: Affymetrix, Inc.
; APPLICANT: Liu, Guoying et al.
; TITLE OF INVENTION: Method of Analysis of Human Polymorphism
; FILE REFERENCE: 3690.1
; CURRENT APPLICATION NUMBER: US/11/175,859
; CURRENT FILING DATE: 2005-07-05
; PRIOR APPLICATION NUMBER: US 60/585,352
; PRIOR FILING DATE: 2004-07-02
; NUMBER OF SEQ ID NOS: 116251
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 97395
; LENGTH: 50
```

```

; TYPE: DNA
; ORGANISM: homo sapien
US-11-175-859-97395

Query Match      70.0%; Score 14; DB 12; Length 50;
Best Local Similarity 87.5%; Pred. No. 9.5e+02;
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      4 CCATATTATGGAATG 19
DB      12 CCTATTATGGAATG 27

RESULT 17
US-10-310-914A-751272
; Sequence 751272, Application US/10310914A
; Publication No. US2006003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuza
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 751272
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-751272

Query Match      69.0%; Score 13.8; DB 8; Length 22;
Best Local Similarity 58.8%; Pred. No. 9.7e+02;
Matches 10; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY      2 CCCCATATTATGGAAT 18
DB      1 CCCCAUUAUUAUGCAU 17

RESULT 18
US-11-121-849-160639
; Sequence 160639, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 160639
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-160639

Query Match      69.0%; Score 13.8; DB 12; Length 25;
Best Local Similarity 88.2%; Pred. No. 1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 TCCCATATTATGGA 17
DB      9 TCCCAATTAATGGA 25

RESULT 19
```



```
APPLICANT: John Palma
TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded s
FILE REFERENCE: 3684.1
CURRENT APPLICATION NUMBER: US/11/121,849
PRIOR APPLICATION NUMBER: 60/567,949
PRIOR FILING DATE: 2004-05-03
NUMBER OF SEQ ID NOS: 673904
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 606251
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapiens
US-11-121-849-606251
```

```
Query Match 71.0%; Score 14.2; DB 12; Length 25;
Best Local Similarity 84.2%; Pred. No. 6.2e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
Oy 2 CCCCATATTATGGAATGA 20
Db 6 CCCCATATGCATGTAATGA 24
```

```
RESULT 11
US-11-101-244-222605/c
Sequence 222605, Application US/11101244
Publication No. US20050246794A1
GENERAL INFORMATION:
APPLICANT: Dharmacon, Inc.
APPLICANT: Khvorova, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 1349905
CURRENT APPLICATION NUMBER: US/11/101,244
PRIOR FILING DATE: 2005-04-07
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 222605
LENGTH: 19
TYPE: RNA
ORGANISM: Homo sapiens
US-11-101-244-222605
```

```
Query Match 70.0%; Score 14; DB 10; Length 19;
Best Local Similarity 100.0%; Pred. No. 7.3e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy 7 TATTTATGGAATGA 20
Db 19 TATTTATGGAATGA 6
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RESULT 12
US-11-101-244-1224663/c
Sequence 1224663, Application US/11101244
Publication No. US20050246794A1
GENERAL INFORMATION:
APPLICANT: Dharmacon, Inc.
APPLICANT: Khvorova, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
```

```
FILE REFERENCE: 1349905
CURRENT APPLICATION NUMBER: US/11/101,244
CURRENT FILING DATE: 2005-04-07
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 1224663
LENGTH: 19
TYPE: RNA
ORGANISM: Homo sapiens
US-11-101-244-1224663
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Query Match 70.0%; Score 14; DB 10; Length 19;
Best Local Similarity 100.0%; Pred. No. 7.3e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Oy 6 ATATTTATGGAATG 19
Db 17 ATATTTATGGAATG 4
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RESULT 13
US-11-083-784-222605/c
Sequence 222605, Application US/11083784
Publication No. US20050245475A1
GENERAL INFORMATION:
APPLICANT: Dharmacon, Inc.
APPLICANT: Khvorova, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 1349905
CURRENT APPLICATION NUMBER: US/11/083,784
CURRENT FILING DATE: 2005-03-18
PRIOR APPLICATION NUMBER: US/10/714,333
PRIOR FILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 222605
LENGTH: 19
TYPE: RNA
ORGANISM: Homo sapiens
US-11-083-784-222605
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Query Match 70.0%; Score 14; DB 11; Length 19;
Best Local Similarity 100.0%; Pred. No. 7.3e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Oy 7 TATTTATGGAATGA 20
Db 19 TATTTATGGAATGA 6
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RESULT 14
US-11-083-784-1224663/c
Sequence 1224663, Application US/11083784
Publication No. US20050245475A1
GENERAL INFORMATION:
APPLICANT: Dharmacon, Inc.
APPLICANT: Khvorova, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
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; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310.914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 113804
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-113804

Query Match
Best Local Similarity 74.0%; Score 14.8; DB 8; Length 22;
Matches 11; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Qy 3 CCCATATTATGGAATGA 20
Db 5 CCAACAUAUUUGGAUAUGA 22

RESULT 6
US-10-310-914A-113805
; Sequence 113805, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 113805
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-113805

Query Match
Best Local Similarity 74.0%; Score 14.8; DB 8; Length 22;
Matches 11; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Qy 3 CCCATATTATGGAATGA 20
Db 5 CCAACAUAUUUGGAUAUGA 22

RESULT 7
US-11-175-859-111867
; Sequence 111867, Application US/11175859
; Publication No. US20060024715A1
; GENERAL INFORMATION:
; APPLICANT: Affymetrix, Inc.
; APPLICANT: Liu, Guoying et al.
; TITLE OF INVENTION: Method of Analysis of Human Polymorphism
; FILE REFERENCE: 3690.1
; CURRENT APPLICATION NUMBER: US/11/175.859
; CURRENT FILING DATE: 2005-07-05
; PRIOR APPLICATION NUMBER: US 60/585.352
; PRIOR FILING DATE: 2004-07-02
; NUMBER OF SEQ ID NOS: 116251
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 111867
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-175-859-111867

Query Match
Best Local Similarity 74.0%; Score 14.8; DB 12; Length 50;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 CCCATATTATGGAATGA 20
Db 5 CCAACAUAUUUGGAUAUGA 22

RESULT 8
US-11-121-849-165142
; Sequence 165142, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121.849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567.949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 165142
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-165142

Query Match
Best Local Similarity 72.0%; Score 14.4; DB 12; Length 25;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 CCATATTATGGAATG 19
Db 9 CCATATTATGGAATG 24

RESULT 9
US-11-136-527-194511/c
; Sequence 194511, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounes, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136.527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574.294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 194511
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Probe
US-11-136-527-194511

Query Match
Best Local Similarity 72.0%; Score 14.4; DB 12; Length 25;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TCCCATATTATGGA 16
Db 18 TCCCATATTATGGA 3

RESULT 10
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; Sequence 606251, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
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94	12.8	64.0	23	8	US-10-310-914A-1307720	Sequence 1307720,
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96	12.8	64.0	25	8	US-10-750-185-18779	Sequence 18779, A
97	12.8	64.0	25	8	US-10-750-623-18779	Sequence 18779, A
98	12.8	64.0	25	12	US-11-121-849-69880	Sequence 69880, A
99	12.8	64.0	25	12	US-11-121-849-216447	Sequence 216447, A
100	12.8	64.0	25	12	US-11-121-849-355721	Sequence 355721, A

ALIGNMENTS

RESULT 1
US-11-175-859-5611/c
; Sequence 5611, Application US/11175859
; Publication No. US20060024715A1
; GENERAL INFORMATION:
; APPLICANT: Affymetrix, Inc.
; APPLICANT: Liu, Guoying et al.
; TITLE OF INVENTION: Method of Analysis of Human Polymorphism
; FILE REFERENCE: 3690.1
; CURRENT APPLICATION NUMBER: US/11/175,859
; CURRENT FILING DATE: 2005-07-05
; PRIOR APPLICATION NUMBER: US 60/585,352
; PRIOR FILING DATE: 2004-07-02
; NUMBER OF SEQ ID NOS: 116251
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5611
; LENGTH: 50
; TYPE: DNA
; ORGANISM: homo sapien
US-11-175-859-5611

Query Match 77.0%; Score 15.4; DB 12; Length 50;
Best Local Similarity 94.1%; Pred. No. 1.7e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TCCCCATTTTATGGA 17
Db 45 TCCCCATTTTATGCA 29

RESULT 2
US-11-175-859-92965/c
; Sequence 92965, Application US/11175859
; Publication No. US20060024715A1
; GENERAL INFORMATION:
; APPLICANT: Affymetrix, Inc.
; APPLICANT: Liu, Guoying et al.
; TITLE OF INVENTION: Method of Analysis of Human Polymorphism
; FILE REFERENCE: 3690.1
; CURRENT APPLICATION NUMBER: US/11/175,859
; CURRENT FILING DATE: 2005-07-05
; PRIOR APPLICATION NUMBER: US 60/585,352
; PRIOR FILING DATE: 2004-07-02
; NUMBER OF SEQ ID NOS: 116251
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 92965
; LENGTH: 50
; TYPE: DNA
; ORGANISM: homo sapien
US-11-175-859-92965

Query Match 76.0%; Score 15.2; DB 12; Length 50;
Best Local Similarity 85.0%; Pred. No. 2.2e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 TCCCCATTTTATGGA 20
Db 25 TCCACATATTTCTGATGA 6

RESULT 3

US-11-024-959-556/c
; Sequence 556, Application US/11024959
; Publication No. US20060010516A1
; GENERAL INFORMATION:
; APPLICANT: FORSTER, RICHARD L.
; APPLICANT: CONNETT, MARIE B.
; APPLICANT: EMERSON, SARAH JANE
; APPLICANT: GRIGOR, MURRAY ROBERT
; APPLICANT: HIGGINS, COLLEEN M.
; APPLICANT: LUND, STEVEN TROY
; APPLICANT: MAGUSIN, ANDREAS
; APPLICANT: KODRZYCKI, BOB
; TITLE OF INVENTION: CELL CYCLE GENES AND RELATED METHODS
; FILE REFERENCE: 044463-0360
; CURRENT APPLICATION NUMBER: US/11/024,959
; CURRENT FILING DATE: 2004-12-30
; PRIOR APPLICATION NUMBER: 60/533,036
; PRIOR FILING DATE: 2003-12-30
; NUMBER OF SEQ ID NOS: 782
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 556
; LENGTH: 60
; TYPE: DNA
; ORGANISM: Eucalyptus sp.
US-11-024-959-556

Query Match 76.0%; Score 15.2; DB 12; Length 60;
Best Local Similarity 85.0%; Pred. No. 2.3e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 TCCCCATTTTATGGA 20
Db 53 TCCCCAACTTATGGAAGA 34

RESULT 4
US-10-310-914A-113803
; Sequence 113803, Application US/10310914A
; Publication No. US2006003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kiyazat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 113803
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-113803

Query Match 74.0%; Score 14.8; DB 8; Length 22;
Best Local Similarity 61.1%; Pred. No. 2.8e+02;
Matches 11; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Qy 3 CCAATTTTATGGA 20
Db 5 CCAACAUUUAUGAUGA 22

RESULT 5
US-10-310-914A-113804
; Sequence 113804, Application US/10310914A
; Publication No. US2006003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kiyazat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 113804
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-113804

Query Match 74.0%; Score 14.8; DB 8; Length 22;
Best Local Similarity 61.1%; Pred. No. 2.8e+02;
Matches 11; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

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13: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	15.4	77.0	50	US-11-175-859-5611	Sequence 5611, Ap
2	15.2	76.0	50	US-11-175-859-92965	Sequence 92965, A
3	15.2	76.0	60	US-11-024-959-556	Sequence 556, App
4	14.8	74.0	22	US-10-310-914A-11803	Sequence 11803, A
5	14.8	74.0	22	US-10-310-914A-11804	Sequence 11804, A
6	14.8	74.0	22	US-10-310-914A-11805	Sequence 11805, A
7	14.8	74.0	50	US-11-175-859-11867	Sequence 11867, A
8	14.4	72.0	25	US-11-121-849-165142	Sequence 165142, A
9	14.4	72.0	25	US-11-136-527-194511	Sequence 194511, A
10	14.2	71.0	25	US-11-121-849-606251	Sequence 606251, A
11	14	70.0	19	US-11-101-244-222605	Sequence 222605, A
12	14	70.0	19	US-11-101-244-122463	Sequence 122463, A
13	14	70.0	19	US-11-083-784-122463	Sequence 222605, A
14	14	70.0	19	US-11-083-784-122463	Sequence 222605, A
15	14	70.0	24	US-10-310-914A-118333	Sequence 118333, A
16	14	70.0	50	US-11-175-859-97395	Sequence 97395, A
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18	13.8	69.0	25	US-11-121-849-160639	Sequence 160639, A
19	13.8	69.0	25	US-11-121-849-216448	Sequence 216448, A
20	13.8	69.0	25	US-11-136-527-228156	Sequence 228156, A

21	13.8	69.0	50	US-11-175-859-31164	Sequence 31164, A
22	13.8	69.0	76	US-10-310-914A-16897	Sequence 16897, A
23	13.6	68.0	25	US-11-121-849-98438	Sequence 98438, A
24	13.6	68.0	25	US-11-121-849-126576	Sequence 126576, A
25	13.6	68.0	25	US-11-121-849-416798	Sequence 416798, A
26	13.6	68.0	50	US-11-175-859-90816	Sequence 90816, A
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28	13.4	67.0	19	US-11-054-047-197	Sequence 197, App1
29	13.4	67.0	12	US-11-054-047-197	Sequence 1285165, A
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31	13.4	67.0	25	US-10-310-914A-1074096	Sequence 1074096, A
32	13.4	67.0	25	US-11-121-849-5217	Sequence 5217, App
33	13.4	67.0	25	US-11-121-849-451249	Sequence 451249, A
34	13.4	67.0	25	US-11-136-527-21556	Sequence 21556, A
35	13.4	67.0	25	US-11-136-527-21557	Sequence 21557, A
36	13.4	67.0	26	US-11-043-755-1024	Sequence 1024, App
37	13.4	67.0	47	US-11-204-311-855	Sequence 855, App
38	13.4	67.0	50	US-11-175-859-76054	Sequence 76054, A
39	13.4	67.0	60	US-11-175-859-104470	Sequence 104470, A
40	13.4	67.0	19	US-10-310-914A-348	Sequence 348, App
41	13.2	66.0	19	US-11-101-244-1056897	Sequence 1056897, A
42	13.2	66.0	19	US-11-083-784-1056897	Sequence 1056897, A
43	13.2	66.0	25	US-10-750-185-9700	Sequence 9700, App
44	13.2	66.0	25	US-10-750-185-9700	Sequence 28001, A
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47	13.2	66.0	25	US-11-121-849-188867	Sequence 188867, A
48	13.2	66.0	25	US-11-121-849-243678	Sequence 243678, A
49	13.2	66.0	25	US-11-121-849-303643	Sequence 303643, A
50	13.2	66.0	25	US-11-136-527-58220	Sequence 58220, A
51	13.2	66.0	25	US-11-136-527-58230	Sequence 58230, A
52	13.2	66.0	25	US-11-136-527-117404	Sequence 117404, A
53	13.2	66.0	25	US-11-136-527-117418	Sequence 117418, A
54	13.2	66.0	25	US-11-136-527-254267	Sequence 254267, A
55	13.2	66.0	26	US-10-310-914A-961364	Sequence 961364, A
56	13.2	66.0	50	US-11-175-859-37290	Sequence 37290, A
57	13.2	66.0	50	US-11-175-859-56314	Sequence 56314, A
58	13.2	66.0	50	US-11-175-859-84841	Sequence 84841, A
59	13.2	66.0	50	US-11-175-859-99109	Sequence 99109, A
60	13.2	66.0	50	US-11-175-859-111776	Sequence 111776, A
61	13.2	66.0	67	US-10-310-914A-12023	Sequence 10203, A
62	13	65.0	19	US-11-101-244-122467	Sequence 122467, A
63	13	65.0	19	US-11-083-784-122467	Sequence 122467, A
64	13	65.0	24	US-10-310-914A-520622	Sequence 520622, A
65	13	65.0	25	US-10-310-914A-520624	Sequence 520624, A
66	13	65.0	12	US-11-101-244-96136	Sequence 96136, A
67	13	65.0	32	US-11-175-859-79849	Sequence 79849, A
68	13	65.0	50	US-11-175-859-25941	Sequence 25941, A
69	13	65.0	50	US-11-175-859-35595	Sequence 35595, A
70	13	65.0	50	US-11-175-859-79439	Sequence 79439, A
71	13	65.0	50	US-11-175-859-102510	Sequence 102510, A
72	13	65.0	50	US-11-175-859-107847	Sequence 107847, A
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74	12.8	64.0	19	US-11-101-244-120585	Sequence 120585, A
75	12.8	64.0	19	US-11-101-244-395533	Sequence 395533, A
76	12.8	64.0	19	US-11-101-244-500910	Sequence 500910, A
77	12.8	64.0	19	US-11-101-244-500910	Sequence 500910, A
78	12.8	64.0	19	US-11-101-244-631486	Sequence 631486, A
79	12.8	64.0	19	US-11-101-244-977070	Sequence 977070, A
80	12.8	64.0	19	US-11-101-244-1052611	Sequence 1052611, A
81	12.8	64.0	19	US-11-101-244-1130904	Sequence 1130904, A
82	12.8	64.0	19	US-11-101-244-1396248	Sequence 1396248, A
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85	12.8	64.0	19	US-11-083-784-500910	Sequence 500910, A
86	12.8	64.0	19	US-11-083-784-631486	Sequence 631486, A
87	12.8	64.0	19	US-11-083-784-977070	Sequence 977070, A
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89	12.8	64.0	19	US-11-083-784-1395533	Sequence 1395533, A
90	12.8	64.0	19	US-11-083-784-1395533	Sequence 1395533, A
91	12.8	64.0	20	US-10-310-914A-181723	Sequence 181723, A
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RESULT 30
US-10-719-956-268246
; Sequence 268246, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 268246
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-268246

```

```

Query Match      68.0%; Score 13.6; DB 7; Length 25;
Best Local Similarity 80.0%; Pred. No. 1.7e+04;
Matches 16; Conservative 0; Mismatches 4; Indels 0;

```

```

QY      1 TCCCCATATTTATGGAATGA 20
        ||||| ||||| |||||
Db      6 TCCCCACATGTATGAATTTA 25

```

Search completed: March 1, 2006, 23:22:53
 Job time : 620.333 secs

```

RESULT 25
; Sequence 357261, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; PRIOR FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 357261
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-357261

```

```

Query Match
Best Local Similarity 69.0%; Score 13.8; DB 8; Length 25;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

QY 4 CCATATTTATGGAATGA 20
    ||||| ||||| |||||
Db 8 CCATATATATGCGATGA 24

```

```

RESULT 26
; Sequence 775584, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; PRIOR FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 775584
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-775584

```

```

Query Match
Best Local Similarity 69.0%; Score 13.8; DB 8; Length 25;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

QY 1 TCCCATATTTATGGA 17
    ||||| ||||| |||||
Db 8 TCCCATATTTATGCA 24

```

```

RESULT 27
US-10-719-900-958681
; Sequence 958681, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; PRIOR FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; NUMBER OF SEQ ID NOS: 982914

```

```

; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 958681
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-958681

```

```

Query Match
Best Local Similarity 69.0%; Score 13.8; DB 8; Length 25;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

QY 2 CCCCATATTTATGGAAT 18
    ||||| ||||| |||||
Db 9 CCCCATATCTGTGGAAT 25

```

```

RESULT 28
US-10-956-157-90813/c
; Sequence 90813, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WI
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; PRIOR FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 90813
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-90813

```

```

Query Match
Best Local Similarity 69.0%; Score 13.8; DB 9; Length 25;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

QY 3 CCCATATTTATGGAATG 19
    ||||| ||||| |||||
Db 25 CCCATATTTATGGAATG 9

```

```

RESULT 29
US-10-956-157-146740
; Sequence 146740, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WI
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; PRIOR FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 146740
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-146740

```

```

Query Match
Best Local Similarity 69.0%; Score 13.8; DB 9; Length 25;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

QY 3 CCCATATTTATGGAATG 19
    ||||| ||||| |||||
Db 5 CCCATATTTATGCGATG 21

```

```

RESULT 20
US-10-786-720-7426/c
; Sequence 7426, Application US/10786720
; Publication No. US2004019181A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: O'Toole, Margot
; APPLICANT: Liu Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING AUTOIMMUNE
; TITLE OF INVENTION: DISEASES
; FILE REFERENCE: 031896-023000 (AM101331L)
; CURRENT APPLICATION NUMBER: US/10/786,720
; CURRENT FILING DATE: 2004-02-26
; NUMBER OF SEQ ID NOS: 21135
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 7426
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-786-720-7426

```

Query Match	69.0%;	Score 13.8;	DB 8;	Length 21;
Best Local Similarity	88.2%;	Pred. No. 1.3e+04;		
Matches	15;	Conservative	0;	Mismatches. 2;
				Indels 0;
				Gaps 0;
QY	3	CCCATATTATGGAATG	19	
Db	17	CCACATTTATGGAATG	1	

```

RESULT 21
US-10-786-720-9676/c
; Sequence 9676, Application US/10786720
; Publication No. US20040191818A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: O'Toole, Margot
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING AUTOIMMUNE
; TITLE OF INVENTION: DISEASES
; FILE REFERENCE: 031896-023000 (AM101331L)
; CURRENT APPLICATION NUMBER: US/10/786,720
; CURRENT FILING DATE: 2004-02-26
; NUMBER OF SEQ ID NOS: 21135
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9676
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-786-720-9676

Query Match          69.0%; Score 13.8; DB 8; Length 21;
Best Local Similarity 88.2%; Pred. No. 1.3e+04;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      3  CCCATATTATGGATG 19
      ||| | ||||| |||
DB      17  CCAACATTATGGATG 1

RESULT 22
US-10-098-2638-4223/c
; Sequence 4223, Application US/100982638
; Publication No. US2003010410A1
; GENERAL INFORMATION:
; APPLICANT: Miltman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,2638
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16

```

```

;
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 4223
;
; LENGTH: 25
;
; TYPE: DNA
; ORGANISM: Homo sapien
; OS-10-098-263B-4223

```

Query Match	69.0%;	Score 13.8;	DB 5;	Length 25;
Best Local Similarity	88.2%;	Pred. No. 1.3e+04;		
Matches 15;	Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0;

Qy 4 CCATATTATGGAATGA 20
||| ||| ||| ||| |||
Db 25 CCATGTTTACGGAATGA 9

RESULT 23
US-10-719

; Sequence 234869, Application US/10719956
; Publication No. US20040146910A1

; GENERAL INFORMATION:

```

;
; APPLICANT: xue mei zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
;

```

```

; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956

```

```

; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836

```

;; PRIOR FILING DATE: 2002 11 20
;; NUMBER OF SEQ ID NOS: 699466

; SOFTWARE: MICROC
; SEQ ID NO 234865

```

; LENGTH: 25
; TYPE: DNA
;

```

ORGANISM: Rattus norvegicus
US-10-719-956-234869

Query Match 69.0%; Score 13.8; DB 7; Length 25;

Best Local Similarity 88.2%; Pred. No. 1.3e+04;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY	1	TCCCATATTATGGA	17
Db	4	TCCCATATTATGGA	20

RESULT 24

US-10-719-956-399696/c

; Sequence 399696, Application US/10/19956
; Publication No. US20040146910A1

; GENERAL INFORMATION:

```

; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
;

```

```

; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956

```

;
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836

; PRIOR FILING DATE: 2002 11 20
 ; NUMBER OF SEQ ID NOS: 699466

```

; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 399696

```

LENGTH: 25
TYPE: DNA

ORGANISM: *Rattus norvegicus* ;
US-10-719-956-399696

```
Query Match      69.0%: Score 13.8: DB 7: Length 252
```

Best Local Similarity	88.2%	Pred. No. 1.3e+04;
Matches	15; Conservative	0; Mismatches 2; Indels 0; Gaps 0;

```

QY      3  CCCATATTATGATG 14
          ||||  |||||
Db      20  CCCAAGTTATGATG 4

```

```

; Sequence 349, Application US/10667236
; Publication No. US20050060764A1
; GENERAL INFORMATION:
; APPLICANT: Susan Gregory
; TITLE OF INVENTION: MOUSE MODEL FOR BONE METABOLISM
; FILE REFERENCE: 23546-8149/B10.0019US
; CURRENT APPLICATION NUMBER: US/10/667,236
; CURRENT FILING DATE: 2003-09-17
; NUMBER OF SEQ ID NOS: 358
; SEQ ID NO 349
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer
US-10-667-236-349

```

```

Query Match      71.0%; Score 14.2; DB 9; Length 25;
Best Local Similarity 84.2%; Pred. No. 8.6e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```

```

QY      2 CCCCATTTTATGGAATGA 20
DB      20 CCCACATTTTATGGAATGA 2

```

```

RESULT 16
US-10-956-157-313397
; Sequence 313397, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 313397
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-313397

```

```

Query Match      71.0%; Score 14.2; DB 9; Length 25;
Best Local Similarity 84.2%; Pred. No. 8.6e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```

```

QY      2 CCCCATTTTATGGAATGA 20
DB      4 CCCCTGATGATGGAATGA 22

```

```

RESULT 17
US-10-944-274-349/C
; Sequence 349, Application US/10944274
; Publication No. US2005014853A1
; GENERAL INFORMATION:
; APPLICANT: Brenda F. Baker
; APPLICANT: C. Frank Bennett
; APPLICANT: Kenneth W. Dobie
; APPLICANT: Kathleen Myers
; APPLICANT: Joshua Finger
; APPLICANT: Lex M. Cowser
; TITLE OF INVENTION: MODULATION OF RANKL EXPRESSION
; FILE REFERENCE: 23546-08148/RTS-0618US
; CURRENT APPLICATION NUMBER: US/10/944,274
; CURRENT FILING DATE: 2004-09-17
; NUMBER OF SEQ ID NOS: 355
; SEQ ID NO 349
; LENGTH: 25

```

```

; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer
US-10-944-274-349

```

```

Query Match      71.0%; Score 14.2; DB 9; Length 25;
Best Local Similarity 84.2%; Pred. No. 8.6e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```

```

QY      2 CCCCATTTTATGGAATGA 20
DB      20 CCCACATTTTATGGAATGA 2

```

```

RESULT 18
US-11-036-317-127081
; Sequence 127081, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 127081
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-127081

```

```

Query Match      71.0%; Score 14.2; DB 10; Length 25;
Best Local Similarity 84.2%; Pred. No. 8.6e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```

```

QY      2 CCCCATTTTATGGAATGA 20
DB      3 CCCGATTTTATGGAATGA 21

```

```

RESULT 19
US-10-719-900-75079
; Sequence 75079, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 75079
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-75079

```

```

Query Match      70.0%; Score 14; DB 8; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      6 ATATTTATGGAATG 19
DB      2 ATATTTATGGAATG 15

```



```
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; Sequence 442498, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002.11.20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 442498
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-442498

Query Match
Best Local Similarity 93.8%; Score 14.4; DB 7; Length 25;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 CCCCATTTTATGGA 17
Db 9 CCCCATTTTATGGA 24

RESULT 11
US-10-719-956-594991/c
; Sequence 594991, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002.11.20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 594991
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-594991

Query Match
Best Local Similarity 93.8%; Score 14.4; DB 7; Length 25;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 CATATTTATGGAATGA 20
Db 24 CATATTTATGGAAGA 9

RESULT 12
US-11-036-317-612570/c
; Sequence 612570, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 612570
; LENGTH: 25
```

```
; TYPE: DNA
; ORGANISM: Mus musculus
; Sequence 379430, Application US/10719900
; Publication No. US2005026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002.11.20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 379430
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-379430

Query Match
Best Local Similarity 84.2%; Score 14.2; DB 8; Length 25;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 CCCCATTTTATGGAATGA 20
Db 20 CCCCATTTTCTGGAAGA 2

RESULT 13
US-10-719-900-379430/c
; Sequence 379430, Application US/10719900
; Publication No. US2005026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002.11.20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 379430
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-379430

Query Match
Best Local Similarity 84.2%; Score 14.2; DB 8; Length 25;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 CATATTTATGGAATGA 20
Db 21 CATATTTATGGAATGA 6
```

```
; TYPE: DNA
; ORGANISM: Mus musculus
; Sequence 632106, Application US/10719900
; Publication No. US2005026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002.11.20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 632106
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-632106

Query Match
Best Local Similarity 84.2%; Score 14.2; DB 8; Length 25;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 TCCCATTTTATGGAATG 19
Db 6 TCAACATTTTATGGAATG 24

RESULT 15
US-10-667-236-349/c
```

Query Match 82.0%; Score 16.4; DB 8; Length 25;
Best Local Similarity 94.4%; Pred. No. 7.7e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CCCCATTATTATGGAATG 19
DB 7 CCCCATTATTATGGAATG 24

RESULT 6

US-10-719-900-705399
; Sequence 705399, Application US/10719900
; Publication No. US20050026164AI
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; PRIOR FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 705399
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-705399

Query Match 74.0%; Score 14.8; DB 8; Length 25;
Best Local Similarity 88.9%; Pred. No. 4.5e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CCCCATTATTATGGAATG 19
DB 7 CCCCATTATTATGGAATG 24

RESULT 7

US-10-672-866-269
; Sequence 269, Application US/10672866
; Publication No. US20050019915AI
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Kenneth Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF SUPEROXIDE DISMUTASE 1,
; TITLE OF INVENTION: SOLUBLE
; FILE REFERENCE: RTS-0242
; CURRENT APPLICATION NUMBER: US/10/672,866
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 10/633,843
; PRIOR FILING DATE: 2003-08-04
; PRIOR APPLICATION NUMBER: 09/888,360
; PRIOR FILING DATE: 2001-06-21
; NUMBER OF SEQ ID NOS: 339
; SEQ ID NO 269
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-672-866-269

Query Match 72.0%; Score 14.4; DB 8; Length 20;
Best Local Similarity 93.8%; Pred. No. 6.7e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCCCATATTATGGA 16
DB 1 TCCCATATTATGGA 16

RESULT 8
US-10-672-866-270
; Sequence 270, Application US/10672866
; Publication No. US20050019915AI
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Kenneth Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF SUPEROXIDE DISMUTASE 1,
; TITLE OF INVENTION: SOLUBLE
; FILE REFERENCE: RTS-0242
; CURRENT APPLICATION NUMBER: US/10/672,866
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 10/633,843
; PRIOR FILING DATE: 2003-08-04
; PRIOR APPLICATION NUMBER: 09/888,360
; PRIOR FILING DATE: 2001-06-21
; NUMBER OF SEQ ID NOS: 339
; SEQ ID NO 270
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-672-866-270

Query Match 72.0%; Score 14.4; DB 8; Length 20;
Best Local Similarity 93.8%; Pred. No. 6.7e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCCCATATTATGGA 16
DB 3 TCCCATATTATGGA 18

RESULT 9

US-10-672-866-271
; Sequence 271, Application US/10672866
; Publication No. US20050019915AI
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Kenneth Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF SUPEROXIDE DISMUTASE 1,
; TITLE OF INVENTION: SOLUBLE
; FILE REFERENCE: RTS-0242
; CURRENT APPLICATION NUMBER: US/10/672,866
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 10/633,843
; PRIOR FILING DATE: 2003-08-04
; PRIOR APPLICATION NUMBER: 09/888,360
; PRIOR FILING DATE: 2001-06-21
; NUMBER OF SEQ ID NOS: 339
; SEQ ID NO 271
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-672-866-271

Query Match 72.0%; Score 14.4; DB 8; Length 20;
Best Local Similarity 93.8%; Pred. No. 6.7e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCCCATATTATGGA 16
DB 5 TCCCATATTATGGA 20

RESULT 10

US-10-719-956-442498

c 97 13 65.0 25 10 US-11-036-317-589091
98 13 65.0 33 9 US-10-891-260-4570
c 99 13 65.0 42 5 US-10-057-890A-27
c 100 13 65.0 42 10 US-11-010-397-27

Sequence 589091,
Sequence 4570, Ap
Sequence 27, Appl
Sequence 27, Appl

ALIGNMENTS

RESULT 1

US-10-173-192-37
; Sequence 37, Application US/10173192
; Publication No. US20030236204A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 2 EXPRESSION
; FILE REFERENCE: PTS-0022
; CURRENT FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 71
; SEQ ID NO 37
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-173-192-37

Query Match 100.0%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TCCCCATTTATGGAATGA 20
Db 1 TCCCCATTTATGGAATGA 20

RESULT 2

US-10-173-192-62/c
; Sequence 62, Application US/10173192
; Publication No. US20030236204A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 2 EXPRESSION
; FILE REFERENCE: PTS-0022
; CURRENT FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 71
; SEQ ID NO 62
; LENGTH: 20
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
US-10-173-192-62

Query Match 100.0%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TCCCCATTTATGGAATGA 20
Db 20 TCCCCATTTATGGAATGA 1

RESULT 3

US-10-653-528-37
; Sequence 37, Application US/10653528
; Publication No. US20040077578A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Kenneth W. Dobie

;; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 2 EXPRESSION
;; FILE REFERENCE: PTS-0022
;; CURRENT APPLICATION NUMBER: US/10/653,528
;; CURRENT FILING DATE: 2003-09-02
;; PRIOR APPLICATION NUMBER: US/10/173,192
;; PRIOR FILING DATE: 2002-06-14
;; NUMBER OF SEQ ID NOS: 71
;; SEQ ID NO 37
;; LENGTH: 20
;; TYPE: DNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Antisense Oligonucleotide
US-10-653-528-37

Query Match 100.0%; Score 20; DB 7; Length 20;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TCCCCATTTATGGAATGA 20
Db 1 TCCCCATTTATGGAATGA 20

RESULT 4

US-10-653-528-62/c
; Sequence 62, Application US/10653528
; Publication No. US20040077578A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 2 EXPRESSION
; FILE REFERENCE: PTS-0022
; CURRENT APPLICATION NUMBER: US/10/653,528
; CURRENT FILING DATE: 2003-09-02
; PRIOR APPLICATION NUMBER: US/10/173,192
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 71
; SEQ ID NO 62
; LENGTH: 20
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
US-10-653-528-62

Query Match 100.0%; Score 20; DB 7; Length 20;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TCCCCATTTATGGAATGA 20
Db 20 TCCCCATTTATGGAATGA 1

RESULT 5

US-10-719-900-705398
; Sequence 705398, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 705398
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-705398

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: March 1, 2006, 22:34:29 ; Search time 617.333 Seconds

(without alignments)
267.906 Million cell updates/sec

Title: US-10-653-528-37

Perfect score: 20

Sequence: 1 tccccatattatgaatga 20

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 11282798

Minimum DB seq length: 0
Maximum DB seq length: 80

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 100 summaries

Database :

Published Applications_NA_Main:*

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- 2: /cgn2_6/prodata/1/pubpna/US08_PUBCOMB.seq:*
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- 10: /cgn2_6/prodata/1/pubpna/US11_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Length	DB	ID	Description
1	20	100.0	20	6	US-10-173-192-37	Sequence 37, Appl
2	20	100.0	20	6	US-10-173-192-62	Sequence 62, Appl
3	20	100.0	20	7	US-10-653-528-37	Sequence 37, Appl
4	20	100.0	20	7	US-10-653-528-62	Sequence 62, Appl
5	16.4	82.0	25	8	US-10-719-900-705398	Sequence 705398,
6	14.8	74.0	25	8	US-10-719-900-705399	Sequence 705399,
7	14.4	72.0	20	8	US-10-672-866-269	Sequence 269, App
8	14.4	72.0	20	8	US-10-672-866-270	Sequence 270, App
9	14.4	72.0	20	8	US-10-672-866-271	Sequence 271, App
10	14.4	72.0	25	7	US-10-719-956-442498	Sequence 442498,
11	14.4	72.0	25	7	US-10-719-956-594991	Sequence 594991,
12	14.4	72.0	25	10	US-11-036-317-612570	Sequence 612570,
13	14.4	71.0	25	8	US-10-719-900-379430	Sequence 379430,
14	14.2	71.0	25	8	US-10-719-900-632106	Sequence 632106,
15	14.2	71.0	25	9	US-10-667-236-349	Sequence 349, App
16	14.2	71.0	25	9	US-10-956-157-313397	Sequence 313397,
17	14.2	71.0	25	10	US-10-944-274-349	Sequence 349, App
18	14.2	71.0	25	10	US-11-036-317-127081	Sequence 127081,
19	14.0	70.0	25	8	US-10-719-900-75079	Sequence 75079, A
20	13.8	69.0	21	8	US-10-786-720-7426	Sequence 7426, Ap
21	13.8	69.0	21	8	US-10-786-720-9676	Sequence 9676, Ap
22	13.8	69.0	25	5	US-10-098-2638-4223	Sequence 4223, Ap
23	13.8	69.0	25	7	US-10-719-956-234869	Sequence 234869,

C 24	13.8	69.0	25	7	US-10-719-956-399696	Sequence 399696,
25	13.8	69.0	25	8	US-10-719-900-357261	Sequence 357261,
26	13.8	69.0	25	8	US-10-719-900-775584	Sequence 775584,
27	13.8	69.0	25	8	US-10-719-900-958681	Sequence 958681,
28	13.8	69.0	25	9	US-10-956-157-90813	Sequence 90813, A
29	13.8	69.0	25	9	US-10-956-157-146740	Sequence 146740,
30	13.6	68.0	25	7	US-10-719-956-268246	Sequence 268246,
31	13.6	68.0	25	8	US-10-719-900-377588	Sequence 377588,
32	13.6	68.0	25	9	US-10-809-189-66318	Sequence 66318, A
33	13.6	68.0	25	9	US-10-843-527-92572	Sequence 92572, A
34	13.6	68.0	25	9	US-10-843-527-145605	Sequence 145605,
35	13.6	68.0	25	10	US-11-036-317-208327	Sequence 208327,
36	13.6	68.0	25	10	US-11-036-317-360898	Sequence 360898,
37	13.6	68.0	40	8	US-10-690-487-820	Sequence 820, App
38	13.6	68.0	50	8	US-10-690-487-812	Sequence 812, App
39	13.6	68.0	65	3	US-09-908-975-26354	Sequence 26354, A
40	13.4	67.0	19	9	US-10-923-475-69	Sequence 26954, A
41	13.4	67.0	19	9	US-10-923-475-197	Sequence 69, Appl
42	13.4	67.0	23	7	US-10-741-601-26183	Sequence 197, App
43	13.4	67.0	23	8	US-10-741-601-73288	Sequence 73288, A
44	13.4	67.0	25	7	US-10-681-773-77501	Sequence 77501, A
45	13.4	67.0	25	8	US-10-719-900-580372	Sequence 580372,
46	13.4	67.0	25	10	US-11-036-317-117871	Sequence 117871, A
47	13.4	67.0	25	10	US-11-036-317-19499	Sequence 19499, A
48	13.4	67.0	25	10	US-11-036-317-19499	Sequence 19499, A
49	13.4	67.0	25	10	US-11-036-317-38069	Sequence 38069, A
50	13.4	67.0	25	10	US-11-036-317-56744	Sequence 56744, A
51	13.4	67.0	25	10	US-11-036-317-582324	Sequence 582324,
52	13.4	67.0	25	10	US-11-036-317-580225	Sequence 580225,
53	13.4	67.0	25	10	US-11-036-317-606610	Sequence 606610,
54	13.4	67.0	25	10	US-11-036-317-681478	Sequence 681478,
55	13.4	67.0	25	10	US-11-036-317-681479	Sequence 681479,
56	13.4	67.0	25	10	US-11-036-317-775539	Sequence 775539,
57	13.4	67.0	47	7	US-10-294-934-855	Sequence 855, App
58	13.4	67.0	71	3	US-09-983-965-208	Sequence 208, App
59	13.2	66.0	20	6	US-10-148-317-15956	Sequence 56, Appl
60	13.2	66.0	20	7	US-10-444-206-391	Sequence 391, App
61	13.2	66.0	20	8	US-10-641-962-391	Sequence 391, App
62	13.2	66.0	25	5	US-10-098-2638-121067	Sequence 121067,
63	13.2	66.0	25	7	US-10-719-956-500592	Sequence 500592,
64	13.2	66.0	25	7	US-10-719-956-595455	Sequence 595455,
65	13.2	66.0	25	8	US-10-719-900-51335	Sequence 51335, A
66	13.2	66.0	25	8	US-10-719-900-280524	Sequence 280524,
67	13.2	66.0	25	8	US-10-719-900-374893	Sequence 374893,
68	13.2	66.0	25	8	US-10-719-900-501976	Sequence 501976,
69	13.2	66.0	25	8	US-10-719-900-637071	Sequence 637071,
70	13.2	66.0	25	8	US-10-719-900-686221	Sequence 686221,
71	13.2	66.0	25	8	US-10-719-900-762907	Sequence 762907,
72	13.2	66.0	25	9	US-10-809-189-66317	Sequence 66317, A
73	13.2	66.0	25	9	US-10-809-189-111261	Sequence 111261,
74	13.2	66.0	25	9	US-10-809-189-118553	Sequence 118553,
75	13.2	66.0	25	9	US-10-956-157-137704	Sequence 137704,
76	13.2	66.0	25	9	US-10-843-527-91113	Sequence 91113, A
77	13.2	66.0	25	9	US-10-843-527-147064	Sequence 147064,
78	13.2	66.0	25	10	US-11-036-317-544045	Sequence 544045,
79	13.2	66.0	25	10	US-11-036-317-593282	Sequence 593282,
80	13.2	66.0	25	10	US-11-036-317-662526	Sequence 662526,
81	13.2	66.0	26	3	US-09-754-853A-1027	Sequence 1027, Ap
82	13.2	66.0	29	9	US-10-489-273-19	Sequence 19, Appl
83	13.2	66.0	41	7	US-10-035-833A-7433	Sequence 7433, Ap
84	13.2	66.0	43	6	US-10-035-833A-791	Sequence 791, App
85	13.2	66.0	45	6	US-10-446-440-1	Sequence 1, Appl1
86	13.2	66.0	45	7	US-10-632-044-1	Sequence 1, Appl1
87	13.2	66.0	45	7	US-10-632-044-1	Sequence 1, Appl1
88	13.2	66.0	45	7	US-10-736-289-1	Sequence 1, Appl1
89	13.2	66.0	47	6	US-10-349-143-723	Sequence 723, Appl
90	13.2	66.0	60	3	US-09-908-975-17295	Sequence 17295, A
91	13.2	66.0	60	9	US-10-764-420-1549	Sequence 1549, Ap
92	13.2	66.0	80	7	US-10-384-245-525	Sequence 525, App
93	13	65.0	18	7	US-10-456-422-28	Sequence 28, Appl
94	13	65.0	25	5	US-10-098-2638-65262	Sequence 65262, A
95	13	65.0	25	7	US-10-719-956-268631	Sequence 268631,
96	13	65.0	25	8	US-10-719-900-357260	Sequence 357260,

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Best Local Similarity 78.9%; Pred. No. 5.1e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 TCCCATATTTATGATG 19
| | | | | | | | | | | | | | | | | | | | |
Db 19 TCCCATATTTAAGATATG 1

Search completed: March 2, 2006, 01:01:36
Job time : 64.333 secs

```
APPLICANT: Schlokat, Uwe
APPLICANT: Falkner, Falko Guenther
APPLICANT: Dornier, Friedrich
TITLE OF INVENTION: An expression plasmid, a fusion protein, a
TITLE OF INVENTION: transfectected eukaryotic cell line, a method of producing foreign
TITLE OF INVENTION: proteins, a foreign protein preparation as well as a pharmaceu
TITLE OF INVENTION: composition
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/557,210A
FILING DATE: 14-NOV-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: A 2099/94
FILING DATE: 14-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: ISACSON, John P.
REGISTRATION NUMBER: 33,715
REFERENCE/DOCKET NUMBER: 040433/0142/SOPA
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 37 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-557-210A-21

Query Match 64.0%; Score 12.8; DB 3; Length 37;
Best Local Similarity 87.5%; Pred. No. 4.4e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TCCCATATTATGGA 16
Db 15 TCCCATATTATGGA 30

RESULT 28
US-10-131-827-3955
Sequence 3955, Application US/10131827
Patent No. 6905827
GENERAL INFORMATION:
APPLICANT: Wohlgemuth, Jay
APPLICANT: Fry, Kirk
APPLICANT: Woodward, Robert
APPLICANT: Ly, Ngoc
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE
TITLE OF INVENTION: CHRONIC INFLAMMATORY DISEASES
FILE REFERENCE: 506612000120
CURRENT APPLICATION NUMBER: US/10/131,827
CURRENT FILING DATE: 2002-09-06
PRIOR APPLICATION NUMBER: US 10/006,290
PRIOR FILING DATE: 2001-10-22
PRIOR APPLICATION NUMBER: US 60/296,764
PRIOR FILING DATE: 2001-06-08
NUMBER OF SEQ ID NOS: 9090
SOFTWARE: PatentIn version 3.1
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SEQ ID NO 3955
LENGTH: 50
TYPE: DNA
ORGANISM: Homo sapiens
US-10-131-827-3955

Query Match 64.0%; Score 12.8; DB 3; Length 50;
Best Local Similarity 87.5%; Pred. No. 4.5e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CCCCATATTATGGA 17
Db 6 CCCCATATTATGGA 21

RESULT 29
US-09-198-452A-4383
Sequence 4383, Application US/09198452A
Patent No. 6559294
GENERAL INFORMATION:
APPLICANT: Griffiths, R.
TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragment
TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prev
FILE REFERENCE: 9710-003-999
CURRENT APPLICATION NUMBER: US/09/198,452A
CURRENT FILING DATE: 1998-11-24
NUMBER OF SEQ ID NOS: 6849
SEQ ID NO 4383
LENGTH: 20
TYPE: DNA
ORGANISM: Chlamydia pneumoniae
US-09-198-452A-4383

Query Match 63.0%; Score 12.6; DB 3; Length 20;
Best Local Similarity 78.9%; Pred. No. 5.1e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 TCCCATATTATGGAATG 19
Db 2 TCCCATATCATAGGAAAG 20

RESULT 30
US-09-422-978-10736/c
Sequence 10736, Application US/09422978
Patent No. 6537751
GENERAL INFORMATION:
APPLICANT: Cohen, Daniel
APPLICANT: Blumenfeld, Marta
APPLICANT: Chumakov, Ilya
TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
FILE REFERENCE: GENSET.020CPI
CURRENT APPLICATION NUMBER: US/09/422,978
CURRENT FILING DATE: 1999-10-20
EARLIER APPLICATION NUMBER: US 09/298,850
EARLIER FILING DATE: 1999-04-21
EARLIER APPLICATION NUMBER: US 60/109,732
EARLIER FILING DATE: 1998-11-23
EARLIER APPLICATION NUMBER: US 60/082,614
EARLIER FILING DATE: 1998-04-21
NUMBER OF SEQ ID NOS: 11796
SEQ ID NO 10736
LENGTH: 21
TYPE: DNA
ORGANISM: Homo Sapiens
FEATURE:
NAME/KEY: primer_bind
LOCATION: 1..21
OTHER INFORMATION: downstream amplification primer 99-19544 for SEQ 2871, in comple
US-09-422-978-10736

Query Match 63.0%; Score 12.6; DB 3; Length 21;
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NAME: Guise, Jeffrey W.
REGISTRATION NUMBER: 34,613
REFERENCE/DOCKET NUMBER: 212/127
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 552-8400
TELEFAX: (619) 552-0159
TELEX: 67-3510
SEQUENCE LISTING
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 31 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-717-888-15
SEQUENCE DESCRIPTION: SEQ ID NO: 15:
Query Match 64.0%; Score 12.8; DB 3; Length 31;
Best Local Similarity 87.5%; Pred. No. 4.3e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 4 CCATATTATGATG 19
DB 2 CCAGATCTATGATG 17
RESULT 25
US-09-491-322-13
Sequence 13, Application US/09491322
Patent No. 6852319
GENERAL INFORMATION:
APPLICANT: Hehn, Mich B.
APPLICANT: Hiatt, Andrew C.
APPLICANT: Ma, Julian K.C.
TITLE OF INVENTION: TRANSGENIC PLANTS EXPRESSING ASSEMBLED
TITLE OF INVENTION: SECRETORY ANTIBODIES
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: THE SCRIPPS RESEARCH INSTITUTE
STREET: 10666 No. 6852319th Torrey Pines Road, TPC-8
City: La Jolla
STATE: California
COUNTRY: US
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/491,322
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/642,406
FILING DATE:
APPLICATION DATA: US 07/427,765
ATTORNEY/AGENT INFORMATION:
NAME: Logan, April C.
REGISTRATION NUMBER: 33,950
REFERENCE/DOCKET NUMBER: 184.2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 554-2937
TELEFAX: (619) 554-6312
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 31 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: NO
ANTI-SENSE: NO
US-09-491-322-13
Query Match 64.0%; Score 12.8; DB 3; Length 31;
Best Local Similarity 87.5%; Pred. No. 4.3e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 4 CCATATTATGATG 19
DB 2 CCAGATCTATGATG 17
RESULT 26
US-08-100-118-12/c
Sequence 12, Application US/08100118
Patent No. 5580773
GENERAL INFORMATION:
APPLICANT: Kang, Chai-Yong
APPLICANT: Luo, Lihong
TITLE OF INVENTION: Design, Construction and Expression
TITLE OF INVENTION: of Chimeric Proteins for Development of AIDS
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merchant & Gould
STREET: 3100 No. 5580773west Center
City: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/100,118
FILING DATE: 19930730
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Strodtloft, Kristine M.
REGISTRATION NUMBER: 34,259
REFERENCE/DOCKET NUMBER: 8692.6-US-01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-332-5300
TELEFAX: 612-332-9081
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: HIV2-gag425
US-08-100-118-12
Query Match 64.0%; Score 12.8; DB 2; Length 33;
Best Local Similarity 87.5%; Pred. No. 4.3e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 3 CCATATTATGATG 18
DB 23 CCATATTATGATG 8
RESULT 27
US-08-557-210A-21
Sequence 21, Application US/08557210A
Patent No. 6114146
GENERAL INFORMATION:
APPLICANT: Herlitschka, Sabine

SECRETORY ANTIBODIES

NUMBER OF SEQUENCES: 26

CORRESPONDENCE ADDRESS:

ADDRESSEE: THE SCRIPPS RESEARCH INSTITUTE

STREET: 10666 No. 6329569th Torrey Pines Road, TPC-8

CITY: La Jolla

STATE: California

COUNTRY: US

ZIP: 92037

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/199,534

FILING DATE: 25-NO. 6329569-1998

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/642,406

FILING DATE: <Unknown>

APPLICATION NUMBER: US 07/427,765

FILING DATE: 27-OCT-1989

ATTORNEY/AGENT INFORMATION:

NAME: Logan, April C.

REGISTRATION NUMBER: 33,950

REFERENCE/DOCKET NUMBER: 184.2

TELECOMMUNICATION INFORMATION:

TELEPHONE: (619) 554-2937

TELEFAX: (619) 554-6312

INFORMATION FOR SEQ ID NO: 13:

SEQUENCE CHARACTERISTICS:

LENGTH: 31 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: NO

ANTI-SENSE: NO

SEQUENCE DESCRIPTION: SEQ ID NO: 13:

US-09-199-534-13

Query Match 64.0%; Score 12.8; DB 3; Length 31;

Best Local Similarity 87.5%; Pred. No. 4.3e+03;

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 CCATATTATGGAATG 19

DB 2 CCAGATCTATGGAATG 17

RESULT 23

US-09-199-534-13

Sequence 13, Application US/09199534

Patent No. 6417429

GENERAL INFORMATION:

APPLICANT: Hein, Mich B.

Hiatt, Andrew C.

Ma, Julian K.C.

TITLE OF INVENTION: TRANSGENIC PLANTS EXPRESSING ASSEMBLED SECRETORY ANTIBODIES

NUMBER OF SEQUENCES: 26

CORRESPONDENCE ADDRESS:

ADDRESSEE: THE SCRIPPS RESEARCH INSTITUTE

STREET: 10666 No. 6417429th Torrey Pines Road, TPC-8

CITY: La Jolla

STATE: California

COUNTRY: US

ZIP: 92037

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/199,534

FILING DATE: 25-NO. 6417429-1998

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/642,406

FILING DATE: <Unknown>

APPLICATION NUMBER: US 07/427,765

FILING DATE: 27-OCT-1989

ATTORNEY/AGENT INFORMATION:

NAME: Logan, April C.

REGISTRATION NUMBER: 33,950

REFERENCE/DOCKET NUMBER: 184.2

TELECOMMUNICATION INFORMATION:

TELEPHONE: (619) 554-2937

TELEFAX: (619) 554-6312

INFORMATION FOR SEQ ID NO: 13:

SEQUENCE CHARACTERISTICS:

LENGTH: 31 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: NO

ANTI-SENSE: NO

SEQUENCE DESCRIPTION: SEQ ID NO: 13:

US-09-199-534-13

Query Match 64.0%; Score 12.8; DB 3; Length 31;

Best Local Similarity 87.5%; Pred. No. 4.3e+03;

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 CCATATTATGGAATG 19

DB 2 CCAGATCTATGGAATG 17

RESULT 24

US-09-717-888-15

Sequence 15, Application US/09717888

Patent No. 6808709

GENERAL INFORMATION:

APPLICANT: ANDREW C. HIATT, JULIAN K.-C. MA, THOMAS LEHNER

TITLE OF INVENTION: IMMUNOGLOBULINS CONTAINING PROTECTION PROTEINS IN PLANTS AND THEIR USES

NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon

STREET: 633 West Fifth Street

Suite 4700

CITY: Los Angeles

STATE: California

COUNTRY: U.S.A.

ZIP: 90071

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage

COMPUTER: IBM Compatible

OPERATING SYSTEM: IBM P.C. DOS 5.0

SOFTWARE: Word Perfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/717,888

FILING DATE: 20-NO. 6808709-2000

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/434,000

FILING DATE: <Unknown>

APPLICATION NUMBER: 08/367,395

FILING DATE: 30-Dec-94

ATTORNEY/AGENT INFORMATION:

Best Local Similarity 72.2%; Pred. No. 3.3e+03;
Matches 13; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 TCCCCATATTATGGAAT 18
Db 21 TCNCCRTANTTNTGGAAT 4

RESULT 16
US-10-057-890A-27/c
; Sequence 27, Application US/10057890A
; Patent No. 6872548
; GENERAL INFORMATION:
; APPLICANT: Coleman, Timothy
; APPLICANT: Mansfield, Brian
; TITLE OF INVENTION: Scaffold Fusion Polypeptides, Composition for Making the Same, and
; FILE REFERENCE: PF537
; CURRENT APPLICATION NUMBER: US/10/057,890A
; CURRENT FILING DATE: 2002-01-29
; PRIOR APPLICATION NUMBER: 60/265,782
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,858
; PRIOR FILING DATE: 2001-01-31
; NUMBER OF SEQ ID NOS: 32
; SEQ ID NO 27
; LENGTH: 42
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotides used to join DNA fragments
US-10-057-890A-27

Query Match 65.0%; Score 13; DB 3; Length 42;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 CCATATTTATGGA 16
Db 22 CCATATTTATGGA 10

RESULT 17
US-09-396-196G-37968
; Sequence 37968, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Miltmann
; APPLICANT: David Lockhart
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 37968
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-37968

Query Match 64.0%; Score 12.8; DB 3; Length 25;
Best Local Similarity 87.5%; Pred. No. 4.2e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TCCCCATATTATGGA 16
Db 9 TCCCCAAATTTCTGGA 24

RESULT 18
US-09-396-196G-120208/c
; Sequence 120208, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Miltmann
; APPLICANT: David Lockhart
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 120208
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-120208

Query Match 64.0%; Score 12.8; DB 3; Length 25;
Best Local Similarity 87.5%; Pred. No. 4.2e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 CATATTTATGGAATGA 20
Db 23 CATGCTTATGGAATGA 8

RESULT 19
US-08-642-406A-13
; Sequence 13, Application US/08642406A
; Patent No. 5959177
; GENERAL INFORMATION:
; APPLICANT: Hein, Mich B.
; APPLICANT: Hiatt, Andrew C.
; APPLICANT: Ma, Julian K.C.
; TITLE OF INVENTION: TRANSGENIC PLANTS EXPRESSING ASSEMBLED
; TITLE OF INVENTION: SECRETORY ANTIBODIES
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESS: THE SCRIPPS RESEARCH INSTITUTE
; STREET: 10666 No. 5959177th Torrey Pines Road, TPC-8
; CITY: La Jolla
; STATE: California
; COUNTRY: US
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/642,406A
; FILING DATE: 03-MAY-1996
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/591,823
; FILING DATE: 02-OCT-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/427,765
; FILING DATE: 27-OCT-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Logan, April C.
; REGISTRATION NUMBER: 33,950
; REFERENCE/DOCKET NUMBER: 184.2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 554-2937
; TELEFAX: (619) 554-6312

RESULT 12
US-09-634-530-17/c
Sequence 17, Application US/09634530
Patent No. 6290958
GENERAL INFORMATION:
APPLICANT: Wisniewski, Nancy
APPLICANT: Silver, Gary M.
APPLICANT: Lo, Katherine C.
APPLICANT: Brandt, Kevin S.
TITLE OF INVENTION: FLEA EXOIDE HYDROLASE PROTEINS AND USES THEREOF
FILE REFERENCE: FC-3-C1-1
CURRENT APPLICATION NUMBER: US/09/634,530
CURRENT FILING DATE: 2000-08-08
PRIOR APPLICATION NUMBER: 09/471,528
PRIOR FILING DATE: 1999-12-27
PRIOR APPLICATION NUMBER: 09/182,816
PRIOR FILING DATE: 1998-10-29
PRIOR APPLICATION NUMBER: 08/989,510
PRIOR FILING DATE: 1997-12-12
NUMBER OF SEQ ID NOS: 35
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 17
LENGTH: 38
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-634-530-17

Query Match 66.0%; Score 13.2; DB 3; Length 38;
Best Local Similarity 83.3%; Pred. No. 2.8e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TCCCATATTATGGAAT 18
DB 23 TCCCATATTATGGAAT 6

RESULT 13
US-09-142-956B-5/c
Sequence 5, Application US/09142956B
Patent No. 6348333
GENERAL INFORMATION:
APPLICANT: Niwa, Mikio
APPLICANT: Okamoto, Masaji
APPLICANT: Matsumoto, Tomoe
APPLICANT: Segawa, Toshiaki
TITLE OF INVENTION: VEGF-BINDING POLYPEPTIDES
FILE REFERENCE: 06501-021001
CURRENT APPLICATION NUMBER: US/09/142,956B
CURRENT FILING DATE: 1999-03-04
PRIOR APPLICATION NUMBER: PCT/JP98/00140
PRIOR FILING DATE: 1998-01-16
PRIOR APPLICATION NUMBER: JP 9/19706
PRIOR FILING DATE: 1997-01-17
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 5
LENGTH: 45
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetically generated primer
US-09-142-956B-5

Query Match 66.0%; Score 13.2; DB 3; Length 45;
Best Local Similarity 83.3%; Pred. No. 2.8e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TCCCATATTATGGAAT 18
DB 25 TCCCATATTATGGAAT 8

RESULT 14
US-09-422-978-723
Sequence 723, Application US/09422978
Patent No. 6537751
GENERAL INFORMATION:
APPLICANT: Cohen, Daniel
APPLICANT: Blumenfeld, Marta
APPLICANT: Chumakov, Ilya
TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
FILE REFERENCE: GENSET-020CPI
CURRENT APPLICATION NUMBER: US/09/422,978
CURRENT FILING DATE: 1999-10-20
EARLIER APPLICATION NUMBER: US 09/298,850
EARLIER FILING DATE: 1999-04-21
EARLIER APPLICATION NUMBER: US 60/109,732
EARLIER FILING DATE: 1998-11-23
EARLIER APPLICATION NUMBER: US 60/082,614
EARLIER FILING DATE: 1998-04-21
NUMBER OF SEQ ID NOS: 11796
SEQ ID NO 723
LENGTH: 47
TYPE: DNA
ORGANISM: Homo Sapiens
FEATURE:
NAME/KEY: allele
LOCATION: 24
OTHER INFORMATION: 99-16847-405 : polymorphic base A or G
US-09-422-978-723

Query Match 66.0%; Score 13.2; DB 3; Length 47;
Best Local Similarity 83.3%; Pred. No. 2.8e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TCCCATATTATGGAAT 18
DB 5 TCCCATATTATGGAAT 22

RESULT 15
US-09-326-806-4/c
Sequence 4, Application US/09326806A
Patent No. 6551793
GENERAL INFORMATION:
APPLICANT: Vainstein, Alexander
APPLICANT: Vishnevsky, Michael
APPLICANT: Ovadis, Marianna
APPLICANT: Itzhaki, Hanan
TITLE OF INVENTION: Carotenoid-Associated Proteins Useful For High
TITLE OF INVENTION: Carotenoid Accumulation And Production In Plants And
TITLE OF INVENTION: Other Organisms
FILE REFERENCE: 59458
CURRENT APPLICATION NUMBER: US/09/326,806A
CURRENT FILING DATE: 1999-06-04
EARLIER APPLICATION NUMBER: PCT/IL97/00399
EARLIER FILING DATE: 1997-12-04
EARLIER APPLICATION NUMBER: 60/032,421
EARLIER FILING DATE: 1996-12-05
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 4
LENGTH: 24
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: synthetic
OTHER INFORMATION: oligonucleotide
OTHER INFORMATION: n = inosine
US-09-326-806-4

Query Match 65.0%; Score 13; DB 3; Length 24;

PRIOR FILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 118553
LENGTH: 25
TYPE: DNA
ORGANISM: mus musculus
US-09-396-196G-118553

Query Match 66.0%; Score 13.2; DB 3; Length 25;
Best Local Similarity 83.3%; Pred. No. 2.6e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TCCCATATTTATGGAAT 18
|||||
DB 25 TCCCATATTTATGAGCAT 8

RESULT 9
US-08-989-510A-16/c
Sequence 16, Application US/08989510A
Patent No. 6037160

GENERAL INFORMATION:

APPLICANT: WISNIEWSKI, Nancy
APPLICANT: SILVER, Gary M.
APPLICANT: LO, Katherine Cailles
APPLICANT: BRANDT, Kevin S.
TITLE OF INVENTION: NOVEL FLEA EPOXIDE HYDROLASE
TITLE OF INVENTION: NUCLEIC ACID MOLECULES, PROTEINS
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Carol Talkington Verser, Ph.D.
ADDRESSEE: Heeska Corporation
STREET: 1825 Sharp Point Drive
CITY: Fort Collins
STATE: Colorado
COUNTRY: USA
ZIP: 80525

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: WordPerfect for Windows, Version 7.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/989,510A
FILING DATE: 12-DEC-1997
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: FC-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 970/493-7272
TELEFAX: 970/484-9505

INFORMATION FOR SEQ ID NO: 16:

SEQUENCE CHARACTERISTICS:
LENGTH: 38 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Primer
US-08-989-510A-16

Query Match 66.0%; Score 13.2; DB 3; Length 38;
Best Local Similarity 83.3%; Pred. No. 2.8e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TCCCATATTTATGGAAT 18
|||||
DB 23 TCCCATATTTATGAGCAT 6

RESULT 10

US-09-182-816-17/c

Sequence 17, Application US/09182816
Patent No. 6143542

GENERAL INFORMATION:

APPLICANT: WISNIEWSKI, Nancy
APPLICANT: SILVER, Gary M.
APPLICANT: LO, Katherine C.
APPLICANT: BRANDT, Kevin S.
TITLE OF INVENTION: NOVEL FLEA EPOXIDE HYDROLASE NUCLEIC ACID MOLECULES,
FILE REFERENCE: FC-3-C1
CURRENT APPLICATION NUMBER: US/09/182,816
CURRENT FILING DATE: 1998-10-29
EARLIER APPLICATION NUMBER: 08/989,510
EARLIER FILING DATE: 1997-12-12
NUMBER OF SEQ ID NOS: 31
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 17
LENGTH: 38
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-182-816-17

Query Match 66.0%; Score 13.2; DB 3; Length 38;
Best Local Similarity 83.3%; Pred. No. 2.8e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TCCCATATTTATGGAAT 18
|||||
DB 23 TCCCATATTTATGAGCAT 6

RESULT 11

US-09-471-528-17/c

Sequence 17, Application US/09471528
Patent No. 6153197

GENERAL INFORMATION:

APPLICANT: WISNIEWSKI, Nancy
APPLICANT: SILVER, Gary M.
APPLICANT: LO, Katherine C.
TITLE OF INVENTION: NOVEL FLEA EPOXIDE HYDROLASE PROTEINS AND USES THEREOF
FILE REFERENCE: FC-3-C1-1
CURRENT APPLICATION NUMBER: US/09/471,528
CURRENT FILING DATE: 1998-12-27
EARLIER APPLICATION NUMBER: 09/182,816
EARLIER FILING DATE: 1998-10-29
EARLIER APPLICATION NUMBER: 08/989,510
EARLIER FILING DATE: 1997-12-12
NUMBER OF SEQ ID NOS: 35
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 17
LENGTH: 38
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-471-528-17

Query Match 66.0%; Score 13.2; DB 3; Length 38;
Best Local Similarity 83.3%; Pred. No. 2.8e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TCCCATATTTATGGAAT 18
|||||
DB 23 TCCCATATTTATGAGCAT 6

TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-040-548-45

Query Match 66.0%; Score 13.2; DB 2; Length 21;
Best Local Similarity 83.3%; Pred. No. 2.6e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TCCCATATTATGAAT 18
DB 19 TCCCATATTATGAAT 2

RESULT 5
US-08-466-344-45/C
Sequence 45, Application US/08466344
Patent No. 5773583
GENERAL INFORMATION:
APPLICANT: Subhame, Vikas P.
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO THE
TITLE OF INVENTION: FUNCTIONAL DOMAINS OF DNA BINDING PROTEINS
NUMBER OF SEQUENCES: 67
CORRESPONDENCE ADDRESS:
ADDRESSER: Arnold, White & Durkee
STREET: 321 No. 5773583th Clark Street, Suite 800
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60610
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,344
FILING DATE: 06-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/040,548
FILING DATE: 31-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Coughlin, Daniel F.
REGISTRATION NUMBER: 36,111
REFERENCE/DOCKET INFORMATION:
TELEPHONE: (312) 744-0090
TELEFAX: (312) 245-4961
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-466-344-45

Query Match 66.0%; Score 13.2; DB 2; Length 21;
Best Local Similarity 83.3%; Pred. No. 2.6e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TCCCATATTATGAAT 18
DB 19 TCCCATATTATGAAT 2

RESULT 6
US-09-396-196G-66317
Sequence 66317, Application US/09396196G
Patent No. 6821724
GENERAL INFORMATION:

APPLICANT: Michael Miltmann
APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
CURRENT APPLICATION NUMBER: US/09/396,196G
CURRENT FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: 60/100,678
PRIOR FILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 66317
LENGTH: 25
TYPE: DNA
ORGANISM: mus musculus
US-09-396-196G-66317

Query Match 66.0%; Score 13.2; DB 3; Length 25;
Best Local Similarity 83.3%; Pred. No. 2.6e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TCCCATATTATGAAT 18
DB 7 TCCTCATATTCGAGT 24

RESULT 7
US-09-396-196G-111261
Sequence 111261, Application US/09396196G
Patent No. 6821724
GENERAL INFORMATION:
APPLICANT: Michael Miltmann
APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
CURRENT APPLICATION NUMBER: US/09/396,196G
CURRENT FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: 60/100,678
PRIOR FILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 111261
LENGTH: 25
TYPE: DNA
ORGANISM: mus musculus
US-09-396-196G-111261

Query Match 66.0%; Score 13.2; DB 3; Length 25;
Best Local Similarity 83.3%; Pred. No. 2.6e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 CCATATTATGAATGA 20
DB 3 CCATATTATGAATGA 20

RESULT 8
US-09-396-196G-118553/C
Sequence 118553, Application US/09396196G
Patent No. 6821724
GENERAL INFORMATION:
APPLICANT: Michael Miltmann
APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
CURRENT APPLICATION NUMBER: US/09/396,196G
CURRENT FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: 60/100,678

98 12 60.0 39 2 US-08-701-339-22 Sequence 22, Appl
c 99 12 60.0 39 3 US-09-099-011A-37 Sequence 37, Appl
c 100 12 60.0 39 3 US-09-098-877B-37 Sequence 37, Appl

ALIGNMENTS

RESULT 1

US-09-396-196G-66318
; Sequence 66318, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Miltmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 66318
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-66318

Query Match 68.0%; Score 13.6; DB 3; Length 25;
Best Local Similarity 80.0%; Pred. No. 1.7e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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Db 1 TCCCATATTTCTGGAGTCA 20

RESULT 2

US-09-671-317-855
; Sequence 855, Application US/09671317
; Patent No. 6528260
; GENERAL INFORMATION:
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; APPLICANT: Bougueteloret, Lydie
; APPLICANT: Cohen, Annick
; TITLE OF INVENTION: BIALLELIC MARKERS RELATED TO GENES INVOLVED IN DRUG METABOLISM
; FILE REFERENCE: 62.US3.CIP
; CURRENT APPLICATION NUMBER: US/09/671,317
; CURRENT FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US 09/536,178
; PRIOR FILING DATE: 2000-03-23
; PRIOR APPLICATION NUMBER: PCT/IB00/00403
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: US 60/126,269
; PRIOR FILING DATE: 1999-03-25
; PRIOR APPLICATION NUMBER: US 60/131,961
; PRIOR FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 977
; SOFTWARE: Patent.pm
; SEQ ID NO 855
; LENGTH: 47
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: allele
; LOCATION: 24
; OTHER INFORMATION: 12-640-325 : polymorphic base T or C
US-09-671-317-855

Query Match 67.0%; Score 13.4; DB 3; Length 47;
Best Local Similarity 82.4%; Pred. No. 2.3e+03;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TCCCATATTTATGGA 17
Db 21 TGCYCATATTTAGGGA 37

RESULT 3

US-09-467-642-56
; Sequence 56, Application US/09467642
; Patent No. 6300132
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Lex M. Cowsett
; TITLE OF INVENTION: ANTISENSE MODULATION OF TELOMERIC REPEAT BINDING FACTOR 2 EXPRE
; FILE REFERENCE: RTS-0106
; CURRENT APPLICATION NUMBER: US/09/467,642
; CURRENT FILING DATE: 1999-12-20
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 56
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-467-642-56

Query Match 66.0%; Score 13.2; DB 3; Length 20;
Best Local Similarity 83.3%; Pred. No. 2.6e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 TCCCATATTTATGGAAT 18
Db 3 TCCCATATTTCTGCACT 20

RESULT 4

US-08-040-548-45/c
; Sequence 45, Application US/08040548
; Patent No. 5763209
; GENERAL INFORMATION:
; APPLICANT: Sukhame, Vikas P.
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO THE
; NUMBER OF SEQUENCES: 67
; CORRESPONDENCE ADDRESS:
; ADDRESS: Arnold, White & Durkee
; STREET: 321 No. 5763209th Clark Street, Suite 800
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60610
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/040,548
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Coughlin, Daniel F.
; REGISTRATION NUMBER: 36,111
; REFERENCE/DOCKET NUMBER: arc0607
; TELEPHONE: (312) 744-0090
; TELEFAX: (312) 245-4961
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 base pairs

GenCore version 5.1.7
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Run on: March 2, 2006, 00:58:14 ; Search time 62.3333 Seconds
(without alignments)
570.341 Million cell updates/sec

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Searched: 1303057 seqs, 888780828 residues

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Maximum DB seq length: 80

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

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9: /cgn2_6/ptodata/1/ina/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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5	13.2	66.0	21	2	US-08-466-344-45 Sequence 45, App1
6	13.2	66.0	25	3	US-09-396-196G-66317 Sequence 66317, A
7	13.2	66.0	25	3	US-09-396-196G-111261 Sequence 111261, A
8	13.2	66.0	25	3	US-09-396-196G-118553 Sequence 118553, A
9	13.2	66.0	38	3	US-08-989-510A-16 Sequence 16, App1
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11	13.2	66.0	38	3	US-09-471-528-17 Sequence 17, App1
12	13.2	66.0	38	3	US-09-634-530-17 Sequence 17, App1
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61	12.2	61.0	54	2	US-08-630-822A-44 Sequence 44, App1
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84	12.2	60.0	35	3	US-08-491-954-86 Sequence 86, App1
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90	12.2	60.0	39	2	US-08-479-275D-58 Sequence 58, App1
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94	12.2	60.0	39	2	US-08-488-271B-59 Sequence 59, App1
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96	12.2	60.0	39	2	US-08-701-339-21 Sequence 21, App1
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TITLE Direct Submission
JOURNAL Submitted (23-OCT-2003) Balzerque S., UMRGV, INRA/CNRS, 2 rue
Castera, Grignon 91067 Paris cedex FRANCE

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PRN sequence.			
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AA762694.1	GI:2812441		
EST.			
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Mus musculus			
ORGANISM			

FEATURES

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ORIGIN

Query Match      66.0%; Score 13.2; DB 1; Length 37;
Best Local Similarity 83.3%; Pred. No. 1.1e+05;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Db      33 TCCCATTTGAGGAAT 16
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              Ephydroidea; Drosophilidae; Drosophila.
REFERENCE    1 (bases 1 to 31)
              Thibault,S.T., Singer,M.A., Miyazaki,W.Y., Mliah,B., Dome,N.A.,
              Singh,C.M., Buchholz,R., Demsky,M., Francis-Liang,H.L.,
              Ryner,L., Cheung,L.M., Chong,A., Erickson,C., Fisher,W.W.,
              Greer,K., Hartouni,S.R., Howie,E., Jakkula,L., Joo,D., Kilpack,K.,
              Lauter,A., Mazzotta,J., Smith,R.D., Stevens,L.M., Stuber,C.,
              Tan,L.R., Ventura,R., Woo,A., Zakrajsek,I., Zhao,L., Chen,F.,
              Swimmer,C., Koczynski,C., Duyk,G., Winberg,M.L. and Margolis,J.
              A complementary transposon tool kit for Drosophila melanogaster
              using P and piggyBac
              Nat. Genet. 36 (3), 283-287 (2004)
14981521
JOURNAL      PUBMED
COMMENT      Contact: Roger A Hoskins
              Berkeley Drosophila Genome Project
              Lawrence Berkeley National Laboratory
              Mailstop 64-121, One Cyclotron Road, Berkeley, CA 94720, USA
              Tel: 510 486 4015
              Fax: 510 486 6798
              Email: Rho@kslbl.gov
              Sequence recovery method was inverse PCR.
              Sequence orientation is forward strand relative to 5' end of
              piggyBac element.
              The piggyBac insertion position is 28 in the 31 bases. This
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                element on either the X or third chromosome. We induced
                transposase expression by immersing bottles in a
                circulating 37°C water bath for a daily (days 3-10 after
                egg-laying) 1-h heat shock. We outcrossed the resulting
                dysgenic males to an isogenic w- strain. New insertions
                were identified on the basis of a change in eye color
                (third chromosome ammunition) or the appearance of w+ male
                progeny (X chromosome ammunition). All lines were mapped
                to a chromosome by standard genetic methods, examined for
                homozygous viability, and used for recovery of flanking
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ORIGIN
Query Match      66.0%; Score 13.2; DB 10; Length 31;
Best Local Similarity 83.3%; Pred. No. 1.1e+05;
Matches 15; Conservativity 0; Mismatches 3; Indels 0; Gaps 0;

QY      3  CCCATATTATGGAATGA 20
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DEFINITION Pan troglodytes DNA, clone: RP43-072D07.TU, genomic survey
sequence.
ACCESSION AG194254
AUTHORS

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VERSION      AG194254.1  GI:45226430
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ORGANISM     Pan troglodytes
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REFERENCE    1
              Park,H., Kim,Y., Kim,S., Han,Y., Woo,T., Park,K., Eun,C.J.,
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              BAC end sequences of library RP-43
              Unpublished
              2 (bases 1 to 31)
              Park,H., Kim,Y., Kim,S., Han,Y., Woo,T., Park,K., Eun,C.J.,
              Hoon,S.T., Chu,M., Kim,H., Joo,S., Kim,C., Song,W. and Yoo,H.
              Direct Submission
              Submitted (07-JAN-2002) Hong-Seog Park, Korea Research Institute of
              Bioscience and Biotechnology (KRIIB), Genome Research Center (GRC);
              52, Oun-dong, Yusong-gu, Daejeon 305-333, Korea
              (E-mail:redstone@mail.kribb.re.kr, URL:http://pns.grc.kribb.re.kr/,
              Tel:82-42-866-7181, Fax:82-42-860-4409)
              Clones are derived from the chimpanzee BAC library RP-43 This BAC
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ORIGIN
Query Match      66.0%; Score 13.2; DB 10; Length 31;
Best Local Similarity 83.3%; Pred. No. 1.1e+05;
Matches 15; Conservativity 0; Mismatches 3; Indels 0; Gaps 0;

QY      2  CCCCATTTTATGGAATG 19
Db      3  CCCCATCTTCTGTGATG 20

RESULT 29
LOCUS     AJ598495          33 bp      DNA      linear      GSS 15-JAN-2004
DEFINITION Arabidopsis thaliana T-DNA flanking sequence, right border, clone
469G03, genomic survey sequence.
ACCESSION AJ598495
VERSION AJ598495.1  GI:37948123
KEYWORDS GSS; right border; T-DNA flanking sequence.
SOURCE   Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
              rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE    1
              Brunaud,V., Balzergue,S., Dubreucq,B., Aubourg,S., Samson,F.,
              Chauvin,S., Bechtold,N., Cryan,C., Derose,R., Pelletier,G.,
              Lepoint,L., Caboche,M. and Lecharny,A.
              T-DNA integration into the Arabidopsis genome depends on sequences
              of pre-insertion sites
              EMBO Rep. 3 (12), 1152-1157 (2002)
12446565
JOURNAL      PUBMED
REFERENCE    2 (bases 1 to 33)
              Balzergue,S.

```

10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 67.0%; Score 13.4; DB 9; Length 35;
Best Local Similarity 93.3%; Pred. No. 8.9e+04;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 5 CATATTATGGAATG 19
|||||
Db 32 CATATTATGGAATG 18

RESULT 25

BM123391

LOCUS 73 bp mRNA linear EST 01-FEB-2002
DEFINITION L0524A08-3 NIA Mouse Newborn Heart cDNA Library Mus musculus cDNA

ACCESSION BM123391
VERSION BM123391.1 GI:17107159

KEYWORDS

SOURCE

ORGANISM

Mus musculus (house mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 73)
Piao, Y., Kargul, G.J., Dudekula, D.B., Qian, Y., Pantano, S., Lim, M.K. and Ko, M.S.H.
Systematic Analyses of NIA Mouse Newborn Heart cDNA Library Unpublished (2001)

CONTACT: Dawood B. Dudekula
Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdna@igsun.gic.nia.nih.gov
Plate: L0524 row: A column: 08
Seq primer: -21M13 Forward
High quality sequence stop: 73
POLYA=yes.

FEATURES

source

Location/Qualifiers
1..73
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:L0524A08-3"
/db_xref="taxon:10090"
/clone="L0524A08"
/tissue_type="Newborn Heart"
/dev_stage="Newborn"
/lab_host="DH10B"
/clone_lib="NIA Mouse Newborn Heart cDNA Library"
/note="Torgan: heart; Vector: pSPORT1 (Invitrogen); Site_1: SalI; Site_2: NotI; Mouse cDNA project by the Laboratory of Genetics, National Institute on Aging (NIA), Intramural Research Program, NIH (http://igsun.gic.nia.nih.gov/cDNA). Double-stranded cDNAs were synthesized with an Oligo(dt) primer (Invitrogen: 5'-
GACAGTCTCTGATCGAGCGCCCTTTTCTTTT-3') from
24.9 microgram of total RNA, created with T4 DNA
polymerase, and purified by ethanol-precipitation. The
cDNAs were ligated to linc- linker L1-Sal3 (Ref.
Development 127:1737-1749 (2000) [PMID: 10725249]),
purified by phenol/chloroform, and separated from free
linkers by Centricon 100. Then, the cDNAs were digested
with SalI and NotI enzymes, and cloned into SalI and NotI

site of pSPORT1 plasmid vector. The DH10B *E. coli* host was transformed with ligation mixture by the chemical method. The average insert size is about 1.8 kb. The library was constructed by Yulan Piao (NIA)."

ORIGIN

Query Match 67.0%; Score 13.4; DB 3; Length 73;
Best Local Similarity 93.3%; Pred. No. 9.5e+04;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 6 ATATTATGGAATGA 20
|||||
Db 21 ATATTATGGAATGA 35

RESULT 26

CL872413

LOCUS 78 bp DNA linear GSS 30-AUG-2004
DEFINITION abe80g07.x1 Soybean methylation filtered genomic library Glycine max genomic, genomic survey sequence.

ACCESSION CL872413
VERSION CL872413.1 GI:51603164

KEYWORDS

SOURCE

ORGANISM

Glycine max (soybean)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseolae; Glycine.
1 (bases 1 to 78)
Nunberg, A., Bedell, J.A., Citek, R.W., Robbins, D., McMenamy, J., Peterson, S., Jones, J., Fries, J., Budiman, M.A., Nguyen, H. and Stacey, G.
Methylation filtered genomic sequences from Glycine max Unpublished (2004)

CONTACT: Gary Stacey
University of Missouri
108 Waters Hall, Columbia, MO 65211, USA
Tel: 573-884-1267
Fax: 573-882-0588
Email: stacey@missouri.edu
LibID: 227
Class: methylation filtered.

FEATURES

source

Location/Qualifiers
1..78
/organism="Glycine max"
/mol_type="genomic DNA"
/cultivar="Williams 82"
/db_xref="taxon:3847"
/tissue_type="Young leaves"
/clone_lib="Soybean methylation filtered genomic library"
/note="Vector: pOT2; Site 1: BstXI; Randomly sheared genomic DNA ranging from 0.7-1.5 kb were end repaired and ligated to BstXI linkers prior to cloning in BstXI-cut pOT2. LibID: 227"

ORIGIN

Query Match 67.0%; Score 13.4; DB 10; Length 78;
Best Local Similarity 93.3%; Pred. No. 9.6e+04;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 4 CCATTTTATGGAAT 18
|||||
Db 58 CCATTTTATGGAAT 72

RESULT 27

CZ469014/c

LOCUS 31 bp DNA linear GSS 29-APR-2005
DEFINITION C04137-Sprime Exelixis p19gyBac PB insertions Drosophila melanogaster genomic Sequence recovered from 5' end of p19gyBac, genomic survey sequence.

ACCESSION

CZ469014

/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0558007"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD2 (gi14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 68.0%; Score 13.6; DB 9; Length 79;
Best Local Similarity 80.0%; Pred. No. 7.7e+04;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 TCCCATATTTCGTAATGA 20
||| ||||| ||||| |||||
46 TTCAATATTCATGTAATGA 27

RESULT 23
CC884465/c
LOCUS
DEFINITION
79 bp DNA linear GSS 31-JUN-2003
SALK_113190.28.40.x Arabidopsis thaliana TDNA insertion lines
Arabidopsis thaliana genomic clone SALK_113190.28.40.x, genomic survey sequence.

ACCESSION
CC884465
VERSION
CC884465.1 GI:33360821
KEYWORDS
GSS.
ORGANISM
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsia.
1 (bases 1 to 79)
Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P., Zimmermann,J. and Ecker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome
Unpublished (2001)
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of TDNA.
Class: TDNA tagged.
Location/Qualifiers
1..79
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/ecotype="Col-0"
/db_xref="taxon:3702"

FEATURES
source

/clone="SALK_113190.28.40.x"
/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/cdna_protocols.html"

ORIGIN

Query Match 68.0%; Score 13.6; DB 9; Length 79;
Best Local Similarity 80.0%; Pred. No. 7.7e+04;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 TCCCATATTTCGTAATGA 20
||| ||||| ||||| |||||
30 TCACCATATTCATGTAATGA 11

RESULT 24
A2761406/c
LOCUS
DEFINITION
35 bp DNA linear GSS 16-FEB-2001
M0555P09R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0555P09 R, genomic survey sequence.

ACCESSION
A2761406
VERSION
A2761406.1 GI:12870292
KEYWORDS
GSS.
ORGANISM
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Muridae; Murinae; Mus.
1 (bases 1 to 35)
Islam,H., Longacre,S., Mahmoud,M., Meenen,B., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., STC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert length: 10000 Std Error: 0.00
Plate: 0555 row: P column: 09
Seq primer: CACACAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 35.
Location/Qualifiers
1..35
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0555P09"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to

FEATURES
source

TITLE Libraries enriched for alternatively spliced exons reveal splicing patterns in melanocytes and melanomas

JOURNAL Nat. Methods 1, 233-239 (2004)

REFERENCE 2 (bases 1 to 74)

AUTHORS Arakawa,T., Carninci,P., Fukuda,S., Harbers,M., Hayatsu,N., Hori,F., Imomani,K., Kondo,S., Morata,M., Nakamura,M., Nomura,K., Ohno,M., Sasaki,D., Shiraki,T., Waki,K., Watanabe,A. and Hayashizaki,Y.

TITLE Direct Submmission

JOURNAL Submitted (15-SEP-2004) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan (E-mail:genome-res@gscc.riken.jp, URL:http://genome-gsc.riken.jp, Tel:81-45-503-9222, Fax:81-45-503-9216)

COMMENT Alternative Splicing Libraries (ASLs) are prepared by: Preparing of single-stranded DNA using a RNA template from full length cDNA libraries, hybridizing of remaining single-stranded DNA, digesting of regions comprising double-stranded DNA by a set of 4 bp-cutters, capturing of DNA hybrids with loop structures (alternative spliced exon), ligation of Y-shaped primers to isolated DNA hybrids with loop structures, PCR amplification of ligation products and their cloning into pUC1 vector. (Reference).

FEATURES Location/Qualifiers

source 1..74

ORIGIN /organism="Mus musculus"

Query Match 68.0%; Score 13.6; DB 4; Length 74;

Best Local Similarity 80.0%; Pred. No. 7.6e+04;

Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

ORIGIN 1 TCCCATTTTATGGAATGA 20

Db 37 TCCATCATGTCATGGAATGA 56

RESULT 21 CG726227 75 bp DNA linear GSS 20-OCT-2003

LOCUS CG726227 1119088H10.y1 1119 - RescueMu Grid AA Zea mays genomic, genomic survey sequence.

DEFINITION CG726227

ACCESSION CG726227.1 GI:37764777

VERSION GSS.

KEYWORDS Zea mays

SOURCE Zea mays

ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoidae; Andropogoneae; Zea.

REFERENCE 1 (bases 1 to 75)

AUTHORS Walbot,V.

TITLE Maize genomic sequences found using engineered RescueMu transposon

JOURNAL Unpublished (2001)

COMMENT Contact: Walbot V

Department of Biological Sciences

Stanford University

855 California Ave, Palo Alto, CA 94304, USA

Tel: 650 723 2227

Fax: 650 725 8221

Email: walbot@stanford.edu

Possible ligation site so sequence was trimmed. Post-ligation

sequence submitted separately.

Plate: 1119088 row: H column: 10

Class: transposon-tagged.

Location/Qualifiers

FEATURES 1..75

source /organism="Zea mays"

ORIGIN /mol_type="genomic DNA"

Query Match 68.0%; Score 13.6; DB 10; Length 75;

Best Local Similarity 80.0%; Pred. No. 7.6e+04;

Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

ORIGIN 1 TCCCATTTTATGGAATGA 20

Db 51 TCCAAATTTTATGGAATGA 32

RESULT 22 AZ763306 79 bp DNA linear GSS 16-FEB-2001

LOCUS AZ763306 1M0558007R Mouse 10kb plasmid UUGCM library Mus musculus genomic clone UUGCM0558007 R, genomic survey sequence.

DEFINITION AZ763306

ACCESSION AZ763306.1 GI:12874201

VERSION GSS.

KEYWORDS Mus musculus (house mouse)

SOURCE Mus musculus

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 79)

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,B., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tinney,A., von Niederhausern,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0558 row: O column: 07

Seq primer: CACACAGAAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 79.

Location/Qualifiers

FEATURES 1..79

source /organism="Mus musculus"

mol_type="genomic DNA"

Arabidopsis Genome
Unpublished (2001)
Contact: Joseph R. Ecker

FEATURES	Location/Qualifiers
source	1. .65

ORIGIN

RESULT 18	
CD998266/c	
LOCUS	71 bp mRNA linear EST 16-JUL-2003
DEFINITION	QBFL1A10.xg QBFL Zea mays cDNA clone QBFL1A10, mRNA sequence.

ORIGIN	—
Query Match	68.0%; Score 13.6; DB 6; Length 71;

```

Qy      1 TCCCATTTTATGGAATGA 20
        || |||||
Db      52 TCTTCATTTTATGGAATCA 33

```

Best Local Similarity 80.0%; Pred. No. 7.6e+04;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

RESULT	19
LOCUS	AY199598
DEFINITION	AY199598 73 bp DNA linear GSS 03-JAN-2005 Arabidopsis thaliana Landsberg DNA Arabidopsis thaliana genomic Clone ET6618.Ds5.12.01.99.b.73, genomic survey sequence.
ACCESSION	AY199598
VERSION	AY199598.1
KEYWORDS	GSS, GI:27895552
SOURCE	Arabidopsis thaliana (thale cress)
ORGANISM	Arabidopsis thaliana

JOURNAL Unpublished (2004)
COMMENT Contact: Martienssen RA

RESULT 20	AK184042	LOCUS	DEFINITION
	AK184042	74 bp	mRNA
			linear
			mus musculus cDNA, clone: Y0G0128F23, strand: minus,
			reference:ENSEMBL:Mouse-Transcript-ENST:ENSMUST00000035194, based
			on BLAT search.

REFERENCE
AUTHORS
1 Watahiki, A., Waki, K., Hayatsu, N., Shiraki, T., Kondô, S., Nakamura, M., Sasaki, D., Arakawa, T., Kawai, J., Harbers, M., Hayahizaki, Y. and Carninci, P.

Query Match 68.0%; Score 13.6; DB 6; Length 57;
Best Local Similarity 80.0%; Pred. No. 7.4e+04;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 TCCCATATTTATGGAATGA 20
| | | | | | | | | | | | | | | | | | | | | |
Db 7 TCCCAAAATTTATGGAACGA 26

RESULT 15
AA152920/c
LOCUS
DEFINITION AA152920 64 bp mRNA linear EST 11-FEB-1997
IMAGE:604635 5', mRNA sequence.
AA152920
VERSION AA152920.1 GI:1724571
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.
1 (bases 1 to 64)
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Geisler, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
Waterston, R.
TITLE The Mashu-HMI Mouse EST Project
JOURNAL Unpublished (1996)
COMMENT Contact: Marra M/Mouse EST Project
Washu-HMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LIND; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:370067
Seq primer: -28m13 rev1 ET from Amerham.

FEATURES
Source Location/Qualifiers
1..64
/organism="Mus musculus"
/mol_type="mRNA"
/strain="NIH Swiss"
/db_xref="taxon:10090"
/clone="IMAGE:604635"
/sex="pooled"
/tissue_type="heart"
/dev_stage="13 day embryo"
/lab_host="SOLR (kanamycin resistant)"
/clone_lib="Stratagene mouse heart (#937316)"
/note="Organ: heart; Vector: plasmid SK-; Site 1:
ECORI; Site 2: XhoI; Cloned unidirectionally. Primer:
Oligo dt. 93 pooled NIH/Swiss 13 day embryo hearts.
Average insert size: 1.0 kb; uni-ZAP XR Vector; ~5'
adaptor sequence: 5' GAATTCGCGACGAG 3' ~3' adaptor
sequence: 5' CTCGAGTTTATTTTATTTT 3'."

ORIGIN
Query Match 68.0%; Score 13.6; DB 1; Length 64;
Best Local Similarity 80.0%; Pred. No. 7.5e+04;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 TCCCATATTTATGGAATGA 20
| | | | | | | | | | | | | | | | | | | | | |
Db 39 TCCCATGTTTGTGACAGCA 20

RESULT 16
B1558013
LOCUS
B1558013 65 bp mRNA linear EST 05-SEP-2001

DEFINITION 603240721F1 NCI_CGAP_Mam4 Mus musculus cDNA clone IMAGE:5293540 5',
mRNA sequence.
ACCESSION B1558013
VERSION B1558013.1 GI:15445327
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.
1 (bases 1 to 65)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Priscilla Furch
Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIND)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LIND at:
<http://image.llnl.gov>
plate: LLAM11742 row: j column: 05
High quality sequence stop: 65.

FEATURES
Source Location/Qualifiers
1..65
/organism="Mus musculus"
/mol_type="mRNA"
/strain="NMRI"
/db_xref="taxon:10090"
/clone="IMAGE:5293540"
/tissue_type="tumor, gross tissue"
/dev_stage="5 months"
/lab_host="DH10B"
/clone_lib="NCI_CGAP Mam4"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: SalI;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.
library constructed by Life Technologies. Investigators
providing samples: Lothar Hennighausen/Priscilla Furch,
NIH Reference for transgenic model: Li et al., Cell Growth
and Differentiation 7, 3-11 (1996)."

ORIGIN
Query Match 68.0%; Score 13.6; DB 3; Length 65;
Best Local Similarity 80.0%; Pred. No. 7.5e+04;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 TCCCATATTTATGGAATGA 20
| | | | | | | | | | | | | | | | | | | | | |
Db 16 TCCCATATTTATTAAGTTA 35

RESULT 17
B2770591
LOCUS
DEFINITION B2770591 65 bp DNA linear GSS 13-MAR-2003
SALK_143526.52.25.n Arabidopsis thaliana TDNA insertion lines
Arabidopsis thaliana genomic clone SALK_143526.52.25.n, genomic
survey sequence.

ACCESSION B2770591
VERSION B2770591.1 GI:28944275
KEYWORDS GSS.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 65)
Alonso, J.M., Leisner, T.J., Barajas, P., Chen, H., Cheuk, R.,
Gadrinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L.,
Shinn, P., Zimmerman, J. and Ecker, J.R.
A Sequence-Indexed Library of Insertion Mutations in the

5' end and NotI at the 3' end.
Vector: pCS107; Site_1: EcoRI; Site_2: NotI
Host: Escherichia coli XL1-blue.
Location/Qualifiers

FEATURES

source

1..79
/organism="Xenopus tropicalis"
/mol_type="mRNA"
/db_xref="taxon:8364"
/clone="TE99038123"
/dev_stage="egg"
/lab_host="Escherichia coli XL1-blue"
/note="Vector: pCS107; Site_1: EcoRI; Site_2: NotI; cDNA was oligo dt primed from 5'ug of poly A+ RNA from egg. EcoRI-NotI cut cDNA was then ligated into pCS107 with EcoRI at the 5' end and NotI at the 3' end"

ORIGIN

Query Match 69.0%; Score 13.8; DB 5; Length 79;
Best Local Similarity 88.2%; Pred. No. 6.1e+04;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CCCCATATTATGAAT 18
|||||
Db 53 CCCCTTTTATGAAT 69

RESULT 13 31 bp DNA linear GSS 02-APR-2002
BH790339 SALK_056850.37.80.x Arabidopsis thaliana TDNA insertion lines
LOCUS Arabidopsis thaliana genomic clone SALK_056850.37.80.x, genomic
DEFINITION survey sequence.

ACCESSION BH790339 GI:19883437
VERSION BH790339
KEYWORDS GSS.

SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 31)

REFERENCE Alonso,J.M., Leisner,T.J., Barajas,P., Chen,H., Cheuk,R.,
Gadri,nab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednisi,L.,
Shim,P., Zimmerman,J. and Becker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the

Arabidopsis Genome
Unpublished (2001)
JOURNAL Contact: Joseph R. Becker

COMMENT

Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ebecker@salk.edu
This is single pass sequence recovered from the left border of
TDNA.
Class: TDNA tagged.

FEATURES

source

Location/Qualifiers
1..31

/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/ecotype="Col-0"
/db_xref="taxon:3702"
/clone="SALK_056850.37.80.x"
/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"

ORIGIN

Query Match 68.0%; Score 13.6; DB 9; Length 31;
Best Local Similarity 80.0%; Pred. No. 7.1e+04;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 TCCCATATTATGAATGA 20
|||||
Db 6 TCTCCACATTATTATGA 25

RESULT 14

CB275155

LOCUS CB275155 57 bp mRNA linear EST 24-FEB-2003
DEFINITION ku58h05.y1 Strongyloides ratti PA female naive SL1 TOPO v2
Strongyloides ratti cDNA 5', mRNA sequence.

ACCESSION CB275155
VERSION CB275155.1 GI:28504751
KEYWORDS EST.

SOURCE Strongyloides ratti
ORGANISM Strongyloides ratti
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
Panagrolaimidae; Strongyloidea; Strongyloides.
1 (bases 1 to 57)

REFERENCE McCarter,J., Clifton,S., Chiapelli,B., Pape,D., Martin,J.,
Wylie,T., Dante,M., Maira,M., Hillier,L., Kucaba,T., Theising,B.,
Bowers,Y., Gibbons,M., Rittler,E., Bennett,J., Franklin,C.,
Tsagarishvili,R., Ronko,I., Kennedy,S., Maguire,L., Beck,C.,
Underwood,K., Steptoe,M., Allen,M., Person,B., Shaller,T.,
Harvey,N., Schurk,R., Kohn,S., Shin,T., Jackson,Y., Cardenas,M.,
McCann,R., Waterston,R. and Wilson,R.
The Washington Univ. Nematode EST Project, 1999
Unpublished (1999)
JOURNAL Contact: McCarter JP

The Washington Univ. Nematode EST Project, 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
The library was constructed by Claire Murphy and Dr. James McCarter
at Washington University, St. Louis. This is a oligo(dT)-SL1 PCR
based library. cDNA PCR products of size >400 nucleotides
containing SL1 on the 5' end and oligo(dT) on the 3' end were
non-directionally cloned into pCRIT-TOPO(Invitrogen) following the
TOPO TA cloning protocol. Parasitic adult females were collected
from immunologically naive animals and provided by Dr. Mark Viney
(Mark.Viney@bristol.ac.uk) of University of Bristol, Bristol, UK.
Putative full length read
The vector to vector length is 58
Seq primer: SL1 primer.

FEATURES

source

Location/Qualifiers
1..57

/organism="Strongyloides ratti"
/mol_type="mRNA"
/db_xref="taxon:34506"
/sex="female"
/dev_stage="Parasitic adult"
/lab_host="DH10B"
/clone_lib="Strongyloides ratti PA female naive SL1 TOPO
v2"
/note="Vector: pCRIT-TOPO (Invitrogen); Site 1: EcoRI;
Site 2: EcoRI; The library was constructed by Claire
Murphy and Dr. James McCarter at Washington University,
St. Louis. This is a oligo(dT)-SL1 PCR based library. cDNA
PCR products of size >400 nucleotides containing SL1 on
the 5' end and oligo(dT) on the 3' end were
non-directionally cloned into pCRIT-TOPO(Invitrogen)
following the TOPO TA cloning protocol. Parasitic adult
females were collected from immunologically naive animals
and provided by Dr. Mark Viney (Mark.Viney@bristol.ac.uk)
of University of Bristol, Bristol, UK."

ORIGIN

was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD2 (g1473214[gbl]AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 69.0%; Score 13.8; DB 9; Length 72;
Best Local Similarity 88.2%; Pred. No. 6.1e+04;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 TCCCATTTTATGGA 17
| | | | | | | | | | | | | | | | | | | | |
Db 31 TACCCAAATTATGGA 15

RESULT 10

CN924729 73 bp mRNA linear EST 07-JUN-2004
LOCUS CN924729
DEFINITION 000415AEIA008286HT (AEIA) Royal Gala young expanding leaf Malus x domestica cDNA AEIA008286, mRNA sequence.

ACCESSION CN924729
VERSION CN924729.1 GI:48397542
KEYWORDS EST.
SOURCE Malus x domestica

ORGANISM Malus x domestica
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids I; Rosales; Rosaceae; Maloideae; Malus.

REFERENCE 1 (bases 1 to 73)
AUTHORS Benning, L., Bowen, J., Crowhurst, R., Gleave, A., Janssen, B., McAtney, S., Newcomb, R., Ross, G., Snowden, K., Walton, E. and Yauk, Y.
TITLE HortResearch Apple EST Project
JOURNAL Unpublished (2004)
COMMENT Contact: Gleave, A.

Sequencing Facility
The Horticulture and Food Research Institute of New Zealand Ltd
120 Mt Albert Rd, Mt Albert, Auckland, New Zealand
Tel: 00 64 09 815 4200
Fax: 00 64 09 815 4201
Email: est@hortresearch.co.nz.

FEATURES
source location/Qualifiers

1..73
/organism="Malus x domestica"
/mol_type="mRNA"
/db_xref="taxon:3750"
/clone="AEIA008286"
/tissue_type="leaf"
/dev_stage="young, expanding"
/clone_lib="(AEIA) Royal Gala young expanding leaf"
/note="Vector: pBK-CMV; library sequenced by Genesis Research & Development"

ORIGIN

Query Match 69.0%; Score 13.8; DB 7; Length 73;
Best Local Similarity 88.2%; Pred. No. 6.1e+04;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 TCCCATTTTATGGA 17
| | | | | | | | | | | | | | | | | | | | |
Db 12 TCCCAAGATTACGAA 28

RESULT 11

D19926 78 bp mRNA linear EST 30-JUN-1996
LOCUS D19926
DEFINITION HMGS00884 Human promyelocyte Homo sapiens cDNA clone mm2371.3', mRNA sequence.

ACCESSION D19926
VERSION D19926.1 GI:500242
KEYWORDS EST.
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae; Homo.

REFERENCE 1 (bases 1 to 78)
AUTHORS Okubo, K., Fukushima, A., Yoshii, J., Niiyama, T., Kojima, Y., Yoshinari, H., Arimoto, J., and Matsubara, K.

Gene expression of human promyelocytic cell line HL60 before and after induction of differentiation. A new application of 3' directed cDNA sequencing

Unpublished (1993)
Contact: Okubo, K., Fukushima, A., Yoshii, J., Niiyama, T., Kojima, Y., Yoshinari, H., Arimoto, J. and Matsubara, K.
Institute for Molecular and Cellular Biology
Osaka University
3-1 Yamada-oka, Suita, Osaka 565, Japan.

FEATURES

source
1..78
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="mm2371"
/clone_lib="human promyelocyte"
/note="Female, adult, cell_line = HL60, cell_type = promyelocyte."

ORIGIN

Query Match 69.0%; Score 13.8; DB 8; Length 78;
Best Local Similarity 88.2%; Pred. No. 6.1e+04;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 3 CCCATTTTATGGAATG 19
| | | | | | | | | | | | | | | | | | | | |
Db 33 CTCACATTATGGAATG 49

RESULT 12
BX783453 79 bp mRNA linear EST 10-DEC-2003
LOCUS BX783453
DEFINITION BX783453 XGC-egg Xenopus tropicalis cDNA clone TB99038f23.3', mRNA sequence.

ACCESSION BX783453
VERSION BX783453.1 GI:39690659
KEYWORDS EST.
SOURCE Xenopus tropicalis (western clawed frog)

ORGANISM Xenopus tropicalis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipridae; Xenopodinae; Xenopus; Silurana.

REFERENCE 1 (bases 1 to 79)
AUTHORS Croning, M.D.R., Ashurst, J.L., Taylor, R., Zorn, A.M. and Rogers, J.
TITLE Sanger Xenopus tropicalis EST project 2001 (11_2003)
JOURNAL Unpublished (2003)

COMMENT Sanger Institute
Sanger Institute
Hinxton, Cambridgeshire, CB10 1SA, UK
Email: trop@sanger.ac.uk
Sanger Xenopus tropicalis EST project 2001
TROPCALIS_SEQUENCE_ID: TB99038f23.q1k17

This sequence is from a Xenopus Gene Collection (XGC) library constructed by Aaron M. Zorn.
cDNA was oligo dt primed from 5ug of poly A+ RNA from egg.
EcoRI-NotI cut cDNA was then ligated into pCS107 with EcoRI at the

/clone.lib="1119 - RescueMu Grid AA"
/note="Organ: leaf; Vector: RescueMu (engineered from pBlueScript backbone); Site 1: BamHI; Site 2: BglII; RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'www.zmdb.iastate.edu' and follow the links for 'RescueMu.' Grid AA was grown at UC San Diego in 2002. DNA was extracted from leaf strips, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."

ORIGIN

Query Match 69.0%; Score 13.8; DB 10; Length 55;
Best Local Similarity 88.2%; Pred. No. 5.9e+04;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 3 CCCATATTATGGAATG 19
18 CTCGAATTATGGAATG 34

RESULT 8 59 bp DNA linear GSS 05-OCT-2000
AZ488165 1M0318J16F Mouse 10kb plasmid UGCGIM library Mus musculus genomic
LOCUS clone UGCGIM0318J16 F, genomic survey sequence.
ACCESSION AZ488165
VERSION AZ488165.1 GI:10656595
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 59)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert length: 10000 Std Error: 0.00
Plate: 0318 row: J column: 16
Seq primer: CGTTGTAAACGACGCGCCACT
Class: plasmid ends
High quality sequence stop: 59.
Location/Qualifiers
1. .59
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCGIM0318J16"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
/clone.lib="Mouse 10kb plasmid UGCGIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a

FEATURES

source

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (G14732114[gb|AF129072.1]), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptor complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 69.0%; Score 13.8; DB 9; Length 59;
Best Local Similarity 88.2%; Pred. No. 6e+04;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 TCCCATATTATGGA 17
3 TCCCATATTATGGA 19

RESULT 9 72 bp DNA linear GSS 04-OCT-2000
AZ471628 1M0286B20F Mouse 10kb plasmid UGCGIM library Mus musculus genomic
LOCUS clone UGCGIM0286B20 F, genomic survey sequence.
ACCESSION AZ471628
VERSION AZ471628.1 GI:10629753
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 72)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert length: 10000 Std Error: 0.00
Plate: 0286 row: B column: 20
Seq primer: CGTTGTAAACGACGCGCCACT
Class: plasmid ends
High quality sequence stop: 72.
Location/Qualifiers
1. .72
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCGIM0286B20"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
/clone.lib="Mouse 10kb plasmid UGCGIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA

FEATURES

source

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (G14732114[gb|AF129072.1]), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptor complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Reverse complemented post-ligation sequence from source sequence.

Plate: 1119064 row: 27
Class: transposon-tagged.

Location/Qualifiers

1. .51

/organism="Zea mays"

/mol_type="genomic DNA"

/cultivar="mixed background W23/A188/B73/K55"

/db_xref="taxon:4577"

/tissue_type="leaf"

/dev_stage="adult"

/lab_host="DH10B"

/clone_lib="1119 - RescueMu Grid AA"

/note="Organ: leaf; Vector: RescueMu (engineered from pBluescript backbone); Site_1: BamHI; Site_2: BglII; RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'www.zmdb.iastate.edu' and follow the links for 'RescueMu'. Grid AA was grown at UC San Diego in 2002. DNA was extracted from leaf strips, double digested with BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."

ORIGIN

Query Match 69.0%; Score 13.8; DB 10; Length 51;

Best Local Similarity 88.2%; Pred. No. 5.9e+04; Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 CCCATATTATGATG 19

Db 19 CTCGAATTATGATG 35

RESULT 6
CR403306 51 bp DNA linear GSS 02-MAY-2004
LOCUS Arabidopsis thaliana T-DNA flanking sequence GK-862C12-025976,
DEFINITION genomic survey sequence.
ACCESSION CR403306 GI:46944034
VERSION CR403306.1 GI:46944034
KEYWORDS GSS.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE
1 Li, Y., Rosso, M.G., Strizhov, N., Viehoever, P., and Weisshaar, B.
GABI-Kat SimpleSearch: a flanking sequence tag (FST) database for
the identification of T-DNA insertion mutants in Arabidopsis
thaliana
JOURNAL Bioinformatics 19 (11), 1441-1442 (2003)
PUBMED 12874060
REFERENCE
2 Rosso, M.G., Li, Y., Strizhov, N., Reiss, B., Dekker, K., and
Weisshaar, B.
An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for
flanking sequence tag-based reverse genetics
JOURNAL Plant Mol. Biol. 53 (1-2), 247-259 (2003)
PUBMED 14756321
REFERENCE
3 Strizhov, N., Li, Y., Rosso, M.G., Viehoever, P., Dekker, K.A. and
Weisshaar, B.
High-throughput generation of sequence indexes from T-DNA
mutagenized Arabidopsis thaliana lines
JOURNAL Biotechniques 35 (6), 1164-1168 (2003)
PUBMED 14682050
REFERENCE
4 (bases 1 to 51)
Strizhov, N., Rosso, M.G., Li, Y. and Weisshaar, B.
Direct Submission

JOURNAL

COMMENT

Submitted (01-MAY-2004) Weisshaar B., Max-Planck-Institut fuer
Zuechtungsforshung, Carl-von-Linn-Wege 10, Koeln, 50829, Germany
This sequence has been recovered from the left border of the T-DNA.
It indicates an insertion close to or within gene Atg30620.
Details on the protocols used for generation of the sequence are
described in References 1-3. The sequences are generated at the MPI
for Plant Breeding Research in the context of the GABI-Kat project.
GABI-Kat is part of the German Plant Genomics program designated
'GABI'. Information on line availability can be found at:
<http://www.mpiz-koeln.mpg.de/GABI-Kat/>.

FEATURES

source

1. .51

/organism="Arabidopsis thaliana"

/mol_type="genomic DNA"

/db_xref="taxon:3702"

/clone="GK-862C12-025976"

/clone_lib="Arabidopsis thaliana T-DNA insertion lines"

/ecotype="Col-0"

/note="PCR was performed on DNA from Arabidopsis thaliana
plants (T1) which were transformed with the T-DNA from
vector pAct161 (Genbank accession number: A537514). The
lines contain one or more T-DNA insertions. The DNA
fragments(s) resulting from the PCR were directly sequenced
to determine the genomic sequence flanking the insertion.
T-DNA derived sequences were removed."

ORIGIN

Query Match 69.0%; Score 13.8; DB 11; Length 51;

Best Local Similarity 88.2%; Pred. No. 5.9e+04; Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TCCCATATTATGAA 17

Db 4 TCCCATATTATGAA 20

RESULT 7
CG720219 55 bp DNA linear GSS 20-OCT-2003
LOCUS 1119061B10.1BL x1 1119 - RescueMu Grid AA Zea mays genomic, genomic
DEFINITION survey sequence.
ACCESSION CG720219 GI:37752897
VERSION CG720219.1 GI:37752897
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE
1 (bases 1 to 55)
Walbot, V.
Maize genomic sequences found using engineered RescueMu transposon
unpublished (2001)
CONTACT Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Very probable ligation site of ends cut by single endonuclease.
Reverse complemented post-ligation sequence from source sequence.
Plate: 1119061 row: 26
Class: transposon-tagged.
Location/Qualifiers
1. .55
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="mixed background W23/A188/B73/K55"
/db_xref="taxon:4577"
/tissue_type="leaf"
/dev_stage="adult"
/lab_host="DH10B"

Query Match 71.0%; Score 14.2; DB 9; Length 27;
Best Local Similarity 84.2%; Pred. No. 3.6e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 TCCCATATTATGATG 19
||||| ||| |||
Db 22 TCCCATATTATTCATG 4

RESULT 3
BH792323
LOCUS
DEFINITION BH792323 48 bp DNA linear GSS 02-Apr-2002
SALK_063412.45.95.x Arabidopsis thaliana TDNA insertion lines
Arabidopsis thaliana genomic clone SALK_063412.45.95.x, genomic
survey sequence.

ACCESSION BH792323
VERSION BH792323.1 GI:19888974
KEYWORDS GSS.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 48)
Alonso,J.M., Leisner,T.J., Barajas,P., Chen,H., Cheuk,R.,
Gadrihab,C., Jeske,A., Karnes,M., Kim,C.U., Parker,H., Prednis,L.,
Shim,P., Zimmerman,J., and Ecker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the
Arabidopsis Genome
Unpublished (2001)
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of
TDNA.
Class: TDNA tagged.

FEATURES
source location/Qualifiers
1..48
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/ecotype="Col-0"
/db_xref="taxon:3702"
/clone="SALK_063412.45.95.x"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"

ORIGIN
Query Match 71.0%; Score 14.2; DB 9; Length 48;
Best Local Similarity 80.0%; Pred. No. 3.8e+04;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 TCCCATATTATGATGA 20
||||| ||| |||
Db 25 TCCCATATTATGATGA 44

RESULT 4
BZ381604
LOCUS
DEFINITION BZ381604 33 bp DNA linear GSS 26-Nov-2002
SALK_116995.26.55.x Arabidopsis thaliana TDNA insertion lines
Arabidopsis thaliana genomic clone SALK_116995.26.55.x, genomic
survey sequence.

ACCESSION BZ381604
VERSION BZ381604.1 GI:25475708

KEYWORDS GSS.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 33)
Alonso,J.M., Leisner,T.J., Barajas,P., Chen,H., Cheuk,R.,
Gadrihab,C., Jeske,A., Karnes,M., Kim,C.U., Parker,H., Prednis,L.,
Shim,P., Zimmerman,J., and Ecker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the
Arabidopsis Genome
Unpublished (2001)
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of
TDNA.
Class: TDNA tagged.

FEATURES
source location/Qualifiers
1..33
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/ecotype="Col-0"
/db_xref="taxon:3702"
/clone="SALK_116995.26.55.x"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"

ORIGIN
Query Match 70.0%; Score 14; DB 9; Length 33;
Best Local Similarity 100.0%; Pred. No. 4.6e+04;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 CATATTATGGAAT 18
||||| ||| |||
Db 19 CATATTATGGAAT 6

RESULT 5
CG720973
LOCUS
DEFINITION CG720973 51 bp DNA linear GSS 20-Oct-2003
1119064608.1EL_x1 1119 - Rescuedu Grid AA Zea mays genomic, genomic
survey sequence.

ACCESSION CG720973
VERSION CG720973.1 GI:37754383
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 51)
Walbot,V.
Maize genomic sequences found using engineered Rescuedu transposon
Unpublished (2001)
Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Very probable ligation site of ends cut by single endonuclease.

	96	12.4	62.0	78	6	CF017073
C 97	12.4	62.0	78	9	AZ793938	
98	12.4	62.0	79	5	BQ541987	
99	12.4	62.0	80	11	CR395349	
C 100	12.2	61.0	19	9	AZ76733	CF017073 QM20D05. A2793938 2M0047A01. BQ541987 ps91f02.y CR395349 Arabidops A276733 2M0010E07

ALIGNMENTS

RESULT 1
A1099326/c
LOCUS
DEFINITION
A1099326 76 bp mRNA linear EST 20-AUG-1998
IMAGE:1482519 5' similar to TR:Q96259 Q96259 AR401. ; mRNA
sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
A1099326.1 GI:3448851
EST.
Mus musculus (house mouse)

REFERENCE
AUTHORS
Marras, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Gelsel, S., Kucaba, T., Lacy, M., Le, M., Martin, V., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
Waterston, R.

TITLE
JOURNAL
COMMENT
The WashU-HMNI Mouse EST Project
Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HMNI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810

Email: mouseest@wustl.wustl.edu
This clone is available royalty-free through LML ; contact the
IMRG Consortium (info@imgc.llnl.gov) for further information.
MGI:930875

Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Seq primer: custom primer used
High quality sequence stop: 1.

FEATURES
SOURCE
Location/Qualifiers
1..76

/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL"
/db_xref="taxon:10090"
/clone="IMAGE:1482519"
/sex="female"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="Sugano mouse liver mlia"
/note="Organ: liver; Vector: pME18S-FU3; Site 1: DraIII
(CACTGCTG) ; Site 2: DraIII (CACCATGTG) ; 1st strand cDNA
was primed with an oligo(dT) primer
[ATGTGACCTTTTCTTTTCTTTT] ; double-stranded cDNA was
ligated to a DraIII adaptor [TGTGGCCTACTG], digested
and cloned into distinct DraIII sites of the pME18S-FU3
vector (5' site CACTGCTG, 3' site CACCATGTG). XhoI should
be used to isolate the cDNA insert. Size selection was
performed to exclude fragments <1.5kb. Library
constructed by Dr. Sumio Sugano (University of Tokyo
Institute of Medical Science). Custom primers for
sequencing: 5' end primer CTTCGCTCTTAAACTGTGG and 3' end
primer CGACCTGCAGCTCGAGCA."

ORIGIN

Query Match

79.0%; Score 15.8; DB 1; Length 76;

Best Local Similarity 89.5%; Pred. No. 6.5e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 TCCCCATATTTTATGGAATG 19
|||||
48 TCCCCATATTTCTTGAATG 30

RESULT 2
A2445616/c
LOCUS
DEFINITION
A2445616 27 bp DNA linear GSS 04-OCT-2000
IMAGE:1M0241G06R Mouse 10kb plasmid UGCM library Mus musculus genomic
clone UGCM0241G06 R, genomic survey sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
A2445616.1 GI:10595614
GSS.
Mus musculus (house mouse)

REFERENCE
AUTHORS
Marras, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Gelsel, S., Kucaba, T., Lacy, M., Le, M., Martin, V., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
Waterston, R.

TITLE
JOURNAL
COMMENT
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0241 row: G column: 06
Seq primer: CACACGAGAAACACTATGACC
Class: plasmid ends
High quality sequence stop: 27.

FEATURES
SOURCE
Location/Qualifiers
1..27

/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCM0241G06"
/sex="male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGCM library"
/note="Vector: pMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (g11473114[gblAF129072.1]), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: March 1, 2006, 22:32:40 ; Search time 2938 Seconds
(without alignments)
318.496 Million cell updates/sec

Title: US-10-653-528-37
Perfect score: 20
Sequence: 1 tccccattatcatgaatga 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapept 1.0

Searched: 41078325 seqs, 23393541228 residues
Total number of hits satisfying chosen parameters: 512758

Minimum DB seq length: 0
Maximum DB seq length: 80

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database :

EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_htc:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_est7:*
9: gb_gss1:*
10: gb_gss2:*
11: gb_gss3:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	15.8	79.0	76	1	AI0993126
C 2	14.2	71.0	27	9	AZ445616
C 3	14.2	71.0	48	9	BH792323
C 4	14	70.0	33	9	BZ381604
5	13.8	69.0	51	10	CG720973
6	13.8	69.0	51	11	CR403306
7	13.8	69.0	55	10	CG720219
8	13.8	69.0	59	9	AZ488165
C 9	13.8	69.0	72	9	AZ471628
10	13.8	69.0	73	7	CN924729
11	13.8	69.0	78	8	DI19926
12	13.8	69.0	79	5	BX783453
13	13.6	68.0	57	6	CB275155
14	13.6	68.0	57	6	BH790339
15	13.6	68.0	64	1	AA152920
16	13.6	68.0	65	3	BI558013
17	13.6	68.0	65	9	BZ770591
C 18	13.6	68.0	71	6	CD998266
19	13.6	68.0	73	9	AI199598
20	13.6	68.0	74	4	AK184042
C 21	13.6	68.0	75	10	CG726227
C 22	13.6	68.0	79	9	AZ763306

C 23	13.6	68.0	79	9	CC884465
C 24	13.4	67.0	35	9	AZ761406
25	13.4	67.0	73	3	BM123391
26	13.4	67.0	78	10	CL872243
C 27	13.2	66.0	31	10	CZ469014
28	13.2	66.0	31	10	AG194254
C 29	13.2	66.0	33	10	AJ598495
C 30	13.2	66.0	37	1	AA762694
C 31	13.2	66.0	44	9	BZ62872
32	13.2	66.0	54	10	AG224626
C 33	13.2	66.0	72	7	CV091494
C 34	13.2	66.0	74	9	AZ462376
C 35	13.2	66.0	77	8	DN839734
C 36	13	65.0	31	9	AZ472852
C 37	13	65.0	57	9	AZ780361
C 38	13	65.0	69	1	AW333728
C 39	13	65.0	70	1	AA681682
40	12.8	64.0	30	9	AZ976292
41	12.8	64.0	34	9	BH740736
42	12.8	64.0	34	10	CZ473738
C 43	12.8	64.0	42	5	C21086
C 44	12.8	64.0	43	1	AA554712
C 45	12.8	64.0	46	1	AA152923
46	12.8	64.0	49	1	AA923178
C 47	12.8	64.0	50	1	AU102232
C 48	12.8	64.0	50	11	DM8546041
C 49	12.8	64.0	52	10	BX949543
C 50	12.8	64.0	55	1	AA923752
C 51	12.8	64.0	55	11	CR293695
52	12.8	64.0	59	3	BM273245
C 53	12.8	64.0	61	1	AI874983
C 54	12.8	64.0	61	10	CG629824
55	12.8	64.0	64	9	BH848104
56	12.8	64.0	67	9	BH846931
C 57	12.8	64.0	68	1	AL658535
C 58	12.8	64.0	69	9	BH225553
59	12.8	64.0	71	6	CB046335
60	12.8	64.0	73	7	CK725864
61	12.8	64.0	76	3	BM354196
62	12.8	64.0	80	6	CD407645
C 63	12.6	63.0	51	9	AZ441063
C 64	12.6	63.0	55	10	CL640822
C 65	12.6	63.0	56	9	AZ608724
C 66	12.6	63.0	58	9	AZ609058
C 67	12.6	63.0	58	10	CL640812
C 68	12.6	63.0	59	6	CB277405
C 69	12.6	63.0	62	9	BH846400
70	12.6	63.0	67	9	BZ384815
71	12.6	63.0	68	5	BY701232
C 72	12.6	63.0	69	7	CN932944
C 73	12.6	63.0	69	10	CG503256
C 74	12.6	63.0	70	1	AI149728
C 75	12.6	63.0	70	6	CD964738
C 76	12.6	63.0	74	5	BQ742866
77	12.6	63.0	75	9	BZ593909
78	12.6	63.0	77	3	BM027453
C 79	12.6	63.0	79	10	CL678271
80	12.6	63.0	79	11	CR552014
C 81	12.6	63.0	80	10	CW293547
C 82	12.4	62.0	33	9	AZ806504
C 83	12.4	62.0	46	9	BH847257
C 84	12.4	62.0	52	11	CR169744
C 85	12.4	62.0	53	5	BX621275
86	12.4	62.0	59	10	BX926231
C 87	12.4	62.0	65	11	CR402624
C 88	12.4	62.0	68	10	CG509580
C 89	12.4	62.0	71	1	AI904673
90	12.4	62.0	71	3	BM269936
C 91	12.4	62.0	75	5	C02514
C 92	12.4	62.0	75	6	CF116298
C 93	12.4	62.0	76	1	AA768859
C 94	12.4	62.0	76	2	BE867849
95	12.4	62.0	77	1	AU259504

CC884465	SAUK_1131
AZ761406	IM0555P09
BM123391	L0524A08-B
CL872243	abe80907.
CZ469014	c04137-5P
AG194254	Pan trogl
AJ598495	Arabidops
AA762694	vv35f06.x
BZ62872	SAUK_0263
AG224626	Lotus cor
CV091494	NA1057_R
AZ462376	IM0269D16
DN839734	SMC-1_06
AZ472852	IM0288B24
AZ780361	2M0017109
AW333728	S25C10_AG
AA681682	vu76e08.r
AZ976292	2M0251110
BH740736	KG01477-5
CZ473738	d04107-3P
CG21086	HUMS000260
AA554712	nk31b02.s
AA152923	mr89h01.r
AA923178	om48a10.s
AU102232	AV102232
AJ546041	Drosophila
BX949543	Arabidops
AA923752	om39f05.s
CR293695	mtel-1M23
BM273245	1f28b03.y
AI874983	u127h03.x
CG629824	OST3h3216
BH848104	SAUK_0675
BH846931	SAUK_0120
AL658535	AL658535
BH225553	1006126H0
CB046335	NISC_gf03
CK725864	SWMB13CAW
BM354196	1f31f01.y
CD407645	Gm_cK3304
AZ441063	IM0232E06
CL640822	M080C05_G
AZ608724	1M0433C09
AZ609058	1M0433D08
CL640812	M077E02_G
CB277405	ku79804.y
BH846400	SAUK_0076
BZ384815	SAUK_1360
BY701232	BX701232
CN932944	000509AOF
CG503256	OST49857
AI149728	tg51c04.x
CD964738	SEP_140_G
BQ742866	baq57404.
BZ593909	SAUK_0824
BM027453	GTT00081
CL678271	PR10122C
CR552014	Forward_B
CW293547	104_774_1
AZ806504	2M0068006
BH847257	SAUK_0507
CR402624	Arabidops
CG509580	OST68089
AI904673	qv-BT065-
BM269936	baK22d11.
C02514	HUMS001240
CF116298	ad154.z1
AA768859	nz75f11.s
BE867849	601443622
AU259504	AU259504

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CC antisense compound is an antisense oligonucleotide which has a modified
CC sugar moiety and nucleobase. The human B7 protein is human B7-1 or B7-2
CC protein or both. The compound is useful for treating airway
CC hyperresponsiveness or pulmonary inflammation, which is associated with
CC asthma, by inhibiting expression of human B7 protein. This sequence
CC represents an antisense oligonucleotide of the invention.

XX
SQ Sequence 20 BP; 7 A; 5 C; 3 G; 5 T; 0 U; 0 Other;

Query Match 66.0%; Score 13.2; DB 12; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.1e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 3 CCCATATTATGGAATGA 20
|||
Db 1 CCCATATPACTTGGAAATGA 18

Search completed: March 1, 2006, 22:51:56
Job time : 342.667 secs

CC of the 5912 nucleic acid sequences or its complement or fragment) with a
CC complementary nucleic acid molecule obtained from the bovine cell, or
CC tissue, where hybridisation between the marker nucleic acid and the
CC complementary nucleic acid permits the detection of the molecule; and (b)
CC detecting the level or pattern of the complementary nucleic acid, where
CC the detection of the complementary nucleic acid is predictive of the
CC level or pattern of the molecule. The LMPD nucleic acid is used for
CC determining a level or pattern of a molecule in a bovine cell or tissue.
CC It is useful for genome mapping, gene identification and analysis, cattle
CC breeding, preparation of constructs for use in cattle gene expression, or
CC for genetically improving cattle. The present sequence is one of the 5912
CC bovine LMPD EST (expressed sequence tag) nucleic acids. Note: The present
CC sequence was not shown in the specification but was obtained in
CC electronic format from the USPTO web site:
CC seqdata.uspto.gov/sequence.html?docid=20020137160
XX
SQ Sequence 71 BP; 25 A; 13 C; 17 G; 16 T; 0 U; 0 Other;

Query Match 67.0%; Score 13.4; DB 8; Length 71;
Best Local Similarity 93.3%; Pred. No. 9.9e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

CC
CY 2 CCCCATATTATGGA 16
DB 29 CCCCATATTATGGA 43

RESULT 29
AAH20687
ID AAH20687 standard; DNA; 20 BP.
XX
AC AAH20687;
XX
DT 13-AUG-2001 (first entry)
XX
DE Human telomeric repeat binding factor 2 oligonucleotide 111415.
XX
KW Antisense; phosphorothioate; human; telomeric repeat binding factor 2;
KW inhibitor; premature aging; hyperproliferative disorder; cancer;
KW cytoskeletal; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT 1..20
FT /*tag= b
FT /mod_base= OTHER
FT /note= "phosphorothioate backbone"
FT 1..3
FT /*tag= a
FT /mod_base= OTHER
FT /note= "2'-O-methoxyethyl"
FT 13..20
FT /*tag= C
FT /mod_base= OTHER
FT /note= "2'-O-methoxyethyl"
XX
PN WO200143752-A1.
XX
PD 21-JUN-2001.
XX
PF 14-DEC-2000; 2000WO-US033954.
XX
PR 17-DEC-1999; 99US-0046642.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Monia BP, Cowsett LM;
XX
DR WPI; 2001-398071/42.
XX
PT Antisense compounds targeted to nucleic acid encoding telomeric repeat
PT binding factor 2 useful for treating conditions such as premature aging

PT and diseases such as cancer.
XX
XX Claim 3; Page 80; 108pp; English.
PS
XX This invention describes a novel antisense compound (I) 8-30 nucleobases
CC in length targeted to a polynucleotide encoding human telomeric repeat
CC binding factor 2 (II) which specifically hybridises with, and inhibits
CC the expression of (II). (I) is useful for treating a human having a
CC disease or condition associated with (II) such as premature aging or a
CC hyperproliferative disorder especially cancer. (I) is useful for
CC expression of (II) in human cells or tissues. (I) is useful for
CC diagnostics, therapeutics, prophylaxis and as research reagents and kits.
CC The products of the invention have cytostatic activity. This sequence
CC represents an antisense oligonucleotide used to illustrate the method of
CC the invention
XX
SQ Sequence 20 BP; 3 A; 8 C; 1 G; 8 T; 0 U; 0 Other;

Query Match 66.0%; Score 13.2; DB 5; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.1e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

CC
CY 1 TCCCATATTATGGAAT 18
DB 3 TCCCATATTATGCACT 20

RESULT 30
ADJ54571
ID ADJ54571 standard; DNA; 20 BP.
XX
AC ADJ54571;
XX
DT 06-MAY-2004 (first entry)
XX
DE Human B7-2 DNA antisense oligonucleotide #186.
XX
KW Airway hyperresponsiveness; pulmonary inflammation;
KW antisense oligonucleotide; human; B7 protein; B7-2; asthma;
KW antiasthmatic; antiinflammatory; ss.
XX
OS Homo sapiens.
XX
FH US2004023917-A1.
FT 05-FEB-2004.
FT 23-MAY-2003; 2003US-00444206.
FT 31-DEC-1996; 96US-00777266.
FT 04-JUN-1999; 99US-00326186.
FT 25-MAY-2000; 2000WO-US014471.
FT 09-MAY-2001; 2001US-00851871.
XX
PA (BENNETT) BENNETT C F.
PA (VICKERS) VICKERS T A.
PA (KARR) KARRAS J G.
XX
PI Bennett CF, Vickers TA, Karras JG;
XX
DR WPI; 2004-132608/13.
XX
PT Treating airway hyperresponsiveness or pulmonary inflammation comprises
PT administering an antisense compound targeted to a nucleic acid molecule
PT encoding a human B7 protein to the individual.
XX
PS Example 27; SEQ ID NO 391; 182pp; English.
XX
XX The invention relates to a method for treating airway hyperresponsiveness
CC or pulmonary inflammation in an individual comprising administering an
CC antisense compound targeted to a nucleic acid molecule encoding a human
CC B7 protein. The invention also relates to a method of inhibiting
CC expression of a nucleic acid molecule encoding B7-1 or B7-2. The

CC neuroprotective, and gastrointestinal-gen. The MLK family kinase
CC inhibitor is useful for the treatment of asthma associated with a risk
CC factor selected from at-risk haplotype for asthma, at-risk haplotype in
CC MAP3K9 gene, polymorphism in MAP3K9 nucleic acid, dysregulation of MAP3K9
CC mRNA expression, dysregulation of MAP3K9 mRNA isoform, increased MLK1
CC protein expression, increased MLK1 biochemical activity and/or increased
CC MLK1 protein isoform expression; and in diagnosis or identification of
CC susceptibility to asthma. The inhibitor is also useful for the treatment
CC of other respiratory diseases associated with MAP3K9 or other members of
CC the JNK pathway such as chronic obstructive pulmonary disease, chronic
CC bronchitis and other inflammatory diseases such as rheumatoid arthritis,
CC psoriasis, multiple sclerosis and inflammatory bowel disease. This
CC polynucleotide sequence represents a forward primer which is used in
CC amplifying a marker of the MAP3K9 kinase, where MAP3K9 is a part of
CC Mitogen-Activated Protein Kinase (MAPK) signal transduction pathways, of
CC the invention.

SO Sequence 26 BP; 7 A; 5 C; 2 G; 12 T; 0 U; 0 Other;

Query Match 67.0%; Score 13.4; DB 14; Length 26;
Best Local Similarity 93.3%; Pred. No. 9.2e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 ATATTATGGAATGA 20
Db 17 ATATTATGGAAGA 3

RESULT 27
AA178771/c
ID AA178771 standard; DNA; 51 BP.
XX
AC AA178771;
XX
DT 09-NOV-2001 (first entry)
XX
DE Human silent SNP containing nucleic acid SEQ:5712.
XX
XX Human; single nucleotide polymorphism; SNP; genome; gene therapy;
KM protein therapy; vaccine; probe; diagnostic assay; detection;
KM quantitation; restorative therapy; polymorphic; ds.
XX
OS Homo sapiens.
XX
PN W0200140521-A2.
XX
PD 07-JUN-2001.
XX
PF 30-NOV-2000; 2000WC-US032758.
XX
PR 30-NOV-1999; 99US-0168138P.
PR 29-NOV-2000; 2000US-00726173.
XX
PA (CURA-) CURAGEN CORP.
XX
XX Shimkets RA, Leach M;
PI
XX WPI; 2001-356160/37.
XX
PT Polymorphic nucleic acid sequences, useful in genetic testing and
PT therapy.
XX
XX Claim 1; Page 2258; 2653pp; English.
PS
XX
CC AA173060 to AA179967 represent isolated human polymorphic polynucleotide
CC sequences (1), which contain single nucleotide polymorphisms (SNPs).
CC AA173114 to AA1753329 represent peptides related to human polymorphic
CC polynucleotide sequences. The sequences can be used in gene and protein
CC therapy, and in vaccine production. (1) and the polypeptides encoded by
CC them may be used in the prevention, diagnosis and treatment of diseases
CC associated with inappropriate expression of polymorphic polypeptides. For
CC example, (1) may be used to treat disorders by rectifying mutations or
CC deletions in a patient's genome that affect the activity of polypeptides

CC by expressing inactive proteins or to supplement the patients own
CC production of polypeptide. Additionally, (1) and its complementary
CC sequences may also be used as DNA probes in diagnostic assays to detect
CC and quantitate the presence of similar nucleic acids in samples, and
CC therefore which patients may be in need of restorative therapy. The
CC polypeptides encoded by (1) may be used as antigens in the production of
CC antibodies specific for polymorphic polypeptides. The antibodies may also
CC be used to down regulate expression and activity. The antibodies may also
CC be used as diagnostic agents for detecting the presence of polymorphic
CC polypeptides in samples

SO Sequence 51 BP; 24 A; 8 C; 7 G; 12 T; 0 U; 0 Other;

Query Match 67.0%; Score 13.4; DB 4; Length 51;
Best Local Similarity 93.3%; Pred. No. 9.7e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 ATATTATGGAATGA 20
Db 27 AGATTATGGAATGA 13

RESULT 28
ABX50279
ID ABX50279 standard; cDNA; 71 BP.
XX
AC ABX50279;
XX
DT 25-FEB-2003 (first entry)
XX
DE Bovine EST associated with lactation/muscle/fat deposition #208.
XX
XX Bovine; ss; EST; expressed sequence tag; lactation; LMPD;
KM muscle deposition; fat deposition; genome mapping; gene identification;
KM gene analysis; cattle breeding.
XX
OS Bos Taurus.
XX
PN US2002137160-A1.
XX
PD 26-SEP-2002.
XX
PF 26-OCT-2001; 2001US-00983965.
XX
PR 17-DEC-1998; 98US-0113678P.
PR 15-DEC-1999; 99US-00465231.
XX
XX (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
XX
PI Byatt JC, Mathialagan N, Tao N, Warren WC;
XX
XX WPI; 2003-102386/09.
XX
PT Purified nucleic acid molecules, useful for genome mapping, gene
PT identification and analysis, cattle breeding or preparation of constructs
PT for cattle gene expression and genetically improved cattle.
XX
XX Claim 2; SEQ ID NO 208; 38pp; English.
PS
XX
CC The invention relates to a purified nucleic acid molecule associated with
CC lactation or muscle and fat deposition (designated LMPD), derived from
CC cattle, and the LMPD nucleic acid can specifically hybridise to a second
CC nucleic acid molecule comprising any of 5912 nucleotide sequences,
CC appearing as ABX50072-ABX5983, or complements of them. Also included are
CC : (1) a transformed cell having a nucleic acid comprising an LMPD nucleic
CC acid linked to a promoter and a 3' non-translated sequence that
CC functions in the cell to cause termination of transcription and addition
CC of polyadenylated ribonucleotides to a 3' end of the mRNA molecule; and
CC (2) determining a level or pattern of a molecule in a bovine cell or
CC tissue comprising: (a) incubating a marker nucleic acid (comprising any

RNA interference; short interfering nucleic acid; siRNA;
 short interfering RNA; siRNA; double-stranded RNA; micro-RNA; miRNA;
 short hairpin RNA; shRNA; expression modulation; gene therapy;
 drug screening; diagnosis; therapeutic target identification;
 pharmacogenomics; gene function analysis; gene mapping; human;
 anti-diabetic; nephrotropic; hepatotropic; cytotoxic;
 transforming growth factor beta receptor; TGFb; TGFb-R;
 diabetic nephropathy; chronic liver disease; pulmonary fibrosis; ss.
 Homo sapiens.
 WO2003070197-A2.
 28-AUG-2003.
 11-FEB-2003; 2003WO-US007273.
 20-FEB-2002; 2002US-0358580P.
 11-MAR-2002; 2002US-0363124P.
 06-JUN-2002; 2002US-0366782P.
 29-AUG-2002; 2002US-0406784P.
 05-SEP-2002; 2002US-0408378P.
 09-SEP-2002; 2002US-0409293P.
 12-NOV-2002; 2002US-0425559P.
 15-JAN-2003; 2003US-0440129P.
 (RIBO-) RIBOZYME PHARM INC.
 Mcswiggen J, Beigelman L;
 WPI: 2003-697557/66.
 New short interfering nucleic acid, useful e.g. for treatment and
 diagnosis of diabetic nephropathy, which downregulates expression of the
 transforming growth factor-beta receptor gene.
 Example 3; SEQ ID NO 197; 137bp; English.
 The invention relates to short interfering nucleic acids (siNA) which
 downregulate expression of the human transforming growth factor beta
 (TGFb) receptor (TGFb-R) gene by RNA interference. The siNAs may or may
 not comprise ribonucleotides and may be double or single stranded. They
 further comprise sense and antisense regions, or alternatively are
 assembled from a sense oligonucleotide and an antisense oligonucleotide.
 Specifically, the siNAs include short interfering RNA (siRNA), double-
 stranded RNA, micro-RNA (miRNA) and short hairpin RNA (shRNA). The siNAs
 can be unmodified or chemically modified, can contain
 deoxyribonucleotides, and can be chemically synthesised, expressed from a
 vector or enzymatically synthesised. The invention also relates to kits
 for the in vitro or in vivo delivery of siNA; conjugates and/or complexes
 of siNA; and vectors that express siNA. The siNAs are used to modulate
 expression of the TGFb-R gene in cells, tissue explants or organisms
 (e.g., by ex vivo gene therapy), or in grafts and transplants for the
 treatment of a variety of conditions. They may be used for treating
 diabetic nephropathy, chronic liver disease or pulmonary fibrosis. The
 siNAs are also useful for drug screening, diagnosis, therapeutic target
 identification and validation, genetic engineering, pharmacogenomics,
 studying gene function, and gene mapping (e.g., of single nucleotide
 polymorphisms). The present sequence represents the lower strand of a
 human TGFb-R-targeted double-stranded siNA.

Sequence 19 BP; 7 A; 2 C; 3 G; 0 T; 7 U; 0 Other;
 Query Match 67.0%; Score 13.4; DB 10; Length 19;
 Best Local Similarity 53.3%; Pred. No. 9e+03;
 Matches 8; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

6 ATATTATGGAATGA 20
 1 AUAUUUAUGGAUACA 15

RESULT 26

ADW81692/c
 ID ADW81692 standard; DNA; 26 BP.
 AC ADW81692;
 DT 07-APR-2005 (first entry)
 DE MAP3K9 marker amplification forward primer #101.
 mixed lineage kinase; MLK; asthma; at-risk haplotype; MAP3K9;
 antiasthmatic; respiratory-gen.; antiinflammatory; antirheumatic;
 antiarthritic; antipsoriatic; neuroprotective; gastrointestinal-gen.;
 respiratory disease; chronic obstructive pulmonary disease;
 chronic bronchitis; inflammation; ss; primer; PCR.
 Unidentified.
 WO2005007144-A2.
 27-JAN-2005.
 14-JUL-2004; 2004WO-US022446.
 14-JUL-2003; 2003US-0487072P.
 05-APR-2004; 2004US-0559611P.
 (DECO-) DECODE GENETICS BHP.
 Hakonarson H, Gurney ME, Halapi E;
 WPI: 2005-122681/13.
 Use of mixed lineage kinase family kinase inhibitor in the manufacture of
 a medicament for treatment of asthma associated at-risk haplotype for
 asthma, at-risk haplotype in MAP3K9 gene or increased MLK1 protein
 expression or activity.
 Disclosure; Fig 12; 640bp; English.
 The invention relates to the novel use of a mixed lineage kinase (MLK)
 family kinase inhibitor for treating asthma. Where the asthma is
 associated with a risk factor selected from an at-risk haplotype for
 asthma, at-risk haplotype in MAP3K9 gene, polymorphism in MAP3K9 nucleic
 acid, dysregulation of MAP3K9 mRNA expression, dysregulation of a MAP3K9
 mRNA isoform, and/or increased MLK1 protein expression. The invention
 further comprises: a method for the diagnosis or identification of
 susceptibility to asthma; a method for the use of a first nucleic acid
 molecule for diagnosing asthma or susceptibility to asthma in a sample;
 a method for assaying the presence of a first nucleic acid molecule in a
 sample; a method for assessing the response to treatment with an MLK
 family kinase nucleic acid inhibitor in a target population or in an
 individual with an at-risk haplotype for asthma, at-risk haplotype in the
 MAP3K9 gene, polymorphism in the MAP3K9 nucleic acid, dysregulation of
 MAP3K9 mRNA expression, dysregulation of MAP3K9 mRNA isoform, increased
 MLK1 protein expression, increased MLK1 biochemical activity or increased
 MLK1 protein isoform expression; a method for assessing the response to
 treatment with an MLK1 inhibitor in a target population including an
 individual with an at-risk haplotype for asthma, as above; a kit for
 assaying a sample for the presence or absence of at least one haplotype
 comprising 2 or more alleles associated with asthma comprising: at least
 one nucleic acid capable of detecting the presence or absence of at least
 one specific allele; a reagent kit for assaying the presence of at least
 one haplotype comprising 2 or more alleles comprising: at least one
 labeled nucleic acid capable of detecting at least one specific allele of
 the haplotype, and reagents for detection of the label; and a reagent kit
 for assaying a sample for the presence of at least one nucleic acid
 comprising 2 or more alleles comprising: at least one nucleic acid
 complementary to at least one nucleotide sequence that is at least partially
 acting as a primer for a primer extension reaction and capable of
 detecting 2 or more specific alleles of the haplotype. The MLK family
 kinase inhibitor has the following activities: antiasthmatic, respiratory
 gen., antiinflammatory, antirheumatic, antiarthritic, antipsoriatic,

```
XX 28-JUN-2000; 2000US-0221607P.
PR 02-MAY-2001; 2001US-0287724P.
XX (COMP-) COMPUGEN INC.
XX Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;
PI WPI; 2002-257383/30.
XX
XX New oligonucleotide libraries comprising oligonucleotides which
PT selectively hybridize to mRNA transcribed from a transcription unit of a
PT genome, useful for detecting tissue-, pathology-, and developmental-
PT specific genes.
XX
XX Example 1; SEQ ID NO 26954; 47pp; English.
XX
XX The present invention describes oligonucleotide libraries for detecting
CC messenger RNAs that populate a (sub-)transcriptome, where the (sub-)
CC )transcriptome comprises messenger RNAs transcribed from multiple
CC )transcription units that populate a genome. The library comprises several
CC oligonucleotides, each capable of hybridizing selectively to a set of
CC messenger RNAs transcribed from a given transcription unit of the genome,
CC which encodes one or more messenger RNA splice variants. The
CC oligonucleotide libraries are useful for detecting mRNAs from a
CC biological sample, in expression profiling studies, in qualitatively or
CC quantitatively characterizing the corresponding transcriptome, and in
CC detecting RNA transcripts and splice variants of human or animal
CC transcriptomes. The libraries may also be used as specialised mini
CC libraries to detect transcripts of a sub-transcriptome under a particular
CC biological or pathological state, and so allowing the detection of tissue
CC - and pathology-specific genes such as those genes only expressed in
CC specific tissue under a specific pathological condition; to detect
CC developmental specific genes; and to detect RNA transcripts and splice
CC variants of a transcriptome of a patient suffering from a particular
CC disorder. ABN27253 to ABN59589 represent oligonucleotide sequences from
CC rats, humans and mice, which are used in the exemplification of the
CC present invention. N.B. The sequence data for this patent did not form
CC part of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 65 BP; 14 A; 18 C; 15 G; 18 T; 0 U; 0 Other;
SQ
XX
XX Query Match 68.0%; Score 13.6; DB 6; Length 65;
XX Best Local Similarity 80.0%; Pred. No. 7.8e+03;
XX Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
XX
XX 1 TCCCCATATTTCGAATGA 20
XX 12 TCCTCATATTTCGAGATCA 31
XX
XX
XX RESULT 24
XX ADJ66231/c
XX ID ADJ66231 standard; RNA; 19 BP.
XX
XX AC ADJ66231;
XX
XX DT 06-MAY-2004 (first entry)
XX
XX DE Human TGFb-R transcript target sequence/siNA upper strand, SEQ ID NO:69.
XX
XX RNA interference; short interfering nucleic acid; siNA;
XX short interfering RNA; siRNA; double-stranded RNA; micro-RNA; miRNA;
XX short hairpin RNA; shRNA; expression modulation; gene therapy;
XX drug screening; diagnosis; therapeutic target identification;
XX pharmacogenomics; gene function analysis; gene mapping; human;
XX anti-diabetic; nephrotropic; hepatotropic; cytostatic;
XX transforming growth factor beta receptor; TGFb; TGFb-R;
XX diabetic nephropathy; chronic liver disease; pulmonary fibrosis;
XX target sequence; se.
XX
XX Homo sapiens.
XX
OS
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XX WO2003070197-A2.
XX
XX 28-AUG-2003.
XX
XX 11-FEB-2003; 2003MO-US007273.
XX
XX 20-FEB-2002; 2002US-0358580P.
XX 11-MAR-2002; 2002US-0363124P.
XX 06-JUN-2002; 2002US-0386782P.
XX 29-AUG-2002; 2002US-0406784P.
XX 05-SEP-2002; 2002US-0408378P.
XX 09-SEP-2002; 2002US-0409293P.
XX 12-NOV-2002; 2002US-0425559P.
XX 15-JAN-2003; 2003US-0440129P.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX
XX Mcswiggen J, Beigelman L;
PI WPI; 2003-697557/66.
XX
XX
XX New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of diabetic neuropathy, which downregulates expression of the
PT transforming growth factor-beta receptor gene.
XX
XX Example 3; SEQ ID NO 69; 137pp; English.
XX
XX The invention relates to short interfering nucleic acids (siNA) which
CC downregulate expression of the human transforming growth factor beta
CC (TGFb) receptor (TGFb-R) gene by RNA interference. The siNAs may or may
CC not comprise ribonucleotides and may be double or single stranded. They
CC further comprise sense and antisense regions, or alternatively are
CC assembled from a sense oligonucleotide and an antisense oligonucleotide.
CC Specifically, the siNAs include short interfering RNA (siRNA), double-
CC stranded RNA, micro-RNA (miRNA) and short hairpin RNA (shRNA). The siNAs
CC can be unmodified or chemically modified, can contain
CC deoxyribonucleotides, and can be chemically synthesised, expressed from a
CC vector or enzymatically synthesised. The invention also relates to kits
CC for the in vitro or in vivo delivery of siNA; conjugates and/or complexes
CC of siNA; and vectors that express siNA. The siNAs are used to modulate
CC expression of the TGFb-R gene in cells, tissue explants or organisms
CC (e.g., by ex vivo gene therapy), or in grafts and transplants for the
CC treatment of a variety of conditions. They may be used for treating
CC diabetic nephropathy, chronic liver disease or pulmonary fibrosis. The
CC siNAs are also useful for drug screening, diagnosis, therapeutic target
CC identification and validation, genetic engineering, pharmacogenomics,
CC studying gene function, and gene mapping (e.g., of single nucleotide
CC polymorphisms). The present sequence represents the upper strand of a
CC human TGFb-R-targeted double-stranded siNA, which is identical to the
CC TGFb-R transcript target sequence.
XX
XX Sequence 19 BP; 7 A; 3 C; 2 G; 0 T; 7 U; 0 Other;
SQ
XX
XX Query Match 67.0%; Score 13.4; DB 10; Length 19;
XX Best Local Similarity 93.3%; Pred. No. 9e+03;
XX Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX 6 ATATTTCGAATGA 20
XX 19 ATATTTCGAATCA 5
XX
XX
XX RESULT 25
XX ADJ66359
XX ID ADJ66359 standard; RNA; 19 BP.
XX
XX AC ADJ66359;
XX
XX DT 06-MAY-2004 (first entry)
XX
XX DE Human TGFb-R siNA lower strand, SEQ ID NO:197.
XX
XX
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XX (RIKE) RIKEN KK.
PA Nakamura Y, Sekine A, Iida A, Saito S;
XX WPI; 2002-583571/62.
XX
DR Identifying individuals having a polymorphism, useful for determining the
PT effectiveness or side effect of a drug or treatment protocol, comprises
PT detecting at least one polymorphism in the drug metabolizing enzyme
PT nucleic acid.
XX
PS Claim 23; Page 218; 2785pp; English.
XX
CC Sequences AB243217-AB250887 represent polymorphic sites within genes
CC encoding enzymes associated with drug metabolism. The invention relates
CC to methods and compositions for identifying individuals who have at least
CC one polymorphism in such drug metabolizing enzyme-encoding genes. The
CC polymorphisms may be identified in a nucleic acid sample using probes or
CC primers specific for a sequence selected from AB243217-AB250887 using a
CC variety of detection assays, including hybridisation assays, nucleic acid
CC arrays and PCR-based methods. The invention also encompasses methods of
CC evaluating and screening drugs using genetic polymorphism data. Genetic
CC polymorphism data, particularly that relating to single nucleotide
CC polymorphisms (SNPs), may be used in studying the relationship between
CC DNA sequence variations and human diseases, conditions, and responses to
CC drugs. SNPs are also useful as polymorphism markers for discovering genes
CC that cause or exacerbate certain diseases. SNPs are particularly useful
CC in the above respects as they are stable in populations, occur
CC frequently, and have lower mutation rates than other genome variations
CC such as repeating sequences. The detection and analysis of polymorphisms
CC in genes encoding drug metabolising enzymes allows the customisation of
CC drug therapies based upon the genetic profile of individual patients.
CC This would not only take the guesswork out of selecting the drug with the
CC greatest therapeutic effect for a particular patient, but would also
CC reduce the likelihood of adverse reactions, thereby increasing safety.
CC Methods of the invention are also useful in the drug discovery and
CC approval processes. For example, individuals could be selected for
CC clinical trials only if their genetic profiles indicate that they are
CC capable of responding to a particular drug or drug class, and previously
CC failed drug candidates could be revived if they were matched with more
CC appropriate patient populations. The methods, data and compositions of
CC the invention may therefore lead to an increase in the range of
CC possible drug targets and decreases in the number of adverse drug
CC reactions, failed drug trials, the time taken for a drug to be approved,
CC the length of time patients are on medication and the number of different
CC medications a patient needs to take before finding an effective therapy
CC
XX
SQ Sequence 41 BP; 14 A; 10 C; 3 G; 14 T; 0 U; 0 Other;
Query Match 68.0%; Score 13.6; DB 6; Length 41;
Best Local Similarity 80.0%; Pred. No. 7.6e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 TCCCCATATTTATGGAATGA 20
Db 9 TCCCATATTCATGACATGA 28
RESULT 20
AA26376
ID AA26376 standard; DNA; 47 BP.
XX
AC AA26376;
XX
DT 10-SEP-2001 (first entry)
XX
DE Human map-related biallelic marker SEQ ID NO:723.
XX
XX Human genome; biallelic marker; high density disequilibrium map;
KW genomic map; haplotype; phenotype; polymorphic base; genotyping;
KW haplotyping; hybridisation; identification; characterisation; diagnosis;
KW single nucleotide polymorphism; SNP; de.

XX Homo sapiens.
OS
XX Key Location/Qualifiers
FH variation replace(24,G)
FT /*tag= a
FT /standard_name= "single nucleotide polymorphism"
FT
PN M09954500-A2.
XX
PD 28-OCT-1999.
XX
XX
XX 21-APR-1999; 99WO-1B00822.
XX
XX 21-APR-1998; 98US-0082614P.
PR 23-NOV-1998; 98US-0109732P.
XX
XX (GEST) GENSET.
PA
PI Cohen D, Blumenfeld M, Chumakov I;
DR WPI; 2000-013267/01.
XX
XX Novel biallelic markers used to construct a high density disequilibrium
PT map of the human genome.
PT
XX
PS Claim 1; Page 384; 2745pp; English.
XX
CC AA265654 to AA269578 represent human biallelic markers from the present
CC invention, which contain a polymorphic base at position 24 of their
CC nucleotide sequences. AA269579 to AA277440 represent amplification
CC primers for the biallelic markers. The biallelic markers of the invention
CC have a variety of uses: they can be used for high density mapping of the
CC human genome, and in complex association studies and haplotyping studies
CC which are useful in determining the genetic basis for disease states.
CC Compositions and methods of the invention can also be useful for the
CC identification of the targets for the development of pharmaceutical
CC agents and diagnostic methods, as well as the characterisation of the
CC differential efficacious responses to and side effects from
CC pharmaceutical agents acting on a disease as well as other treatment.
CC N.B. The SEQ ID NOS 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and
CC 3367, are not actually given a sequence in the Sequence Listing from the
CC present invention
CC
XX
SQ Sequence 47 BP; 14 A; 9 C; 7 G; 17 T; 0 U; 0 Other;
Query Match 68.0%; Score 13.6; DB 3; Length 47;
Best Local Similarity 80.0%; Pred. No. 7.6e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 TCCCCATATTTATGGAATGA 20
Db 5 TCCCCATATTTAAGATTGA 24
RESULT 21
ADS92006/c
ID ADS92006 standard; DNA; 50 BP.
XX
AC ADS92006;
XX
DT 02-DEC-2004 (first entry)
XX
DE DNA oligo capture probe gene78.m0103.
XX
XX biostability; cancer; cytostatic; diagnostic microarray; ss; probe;
KW locked nucleic acid; LNA..
XX
XX Unidentified.
OS
XX
XX Key Location/Qualifiers
FH modified_base 1
FT /*tag= a

```
AC AAT19807;
XX
XX 12-JUL-1996 (first entry)
XX
XX Human gene signature HUMGS00884.
XX
XX Gene signature; messenger RNA; mRNA; relative abundance; frequency;
XX human; cloning; mapping; non-biased library; diagnosis; detection;
XX cell typing; abnormal cell function; ss.
XX
XX Homo sapiens.
XX
XX M09514772-A1.
XX
XX 01-JUN-1995.
XX
XX 11-NOV-1994; 94MO-JP001916.
XX
XX 12-NOV-1993; 93JP-00355504.
XX
XX (MATS/) MATSUBARA K.
XX (OKUB/) OKUBO K.
XX
XX Matsubara K, Okubo K;
XX
XX WPI; 1995-206931/27.
XX
XX Single-stranded DNA for identifying gene signatures - isolated from 3'-
XX directed human cDNA library that reflects relative abundance of corresp.
XX mRNA in specific human tissues.
XX
XX Claim 1; Page 476; 2245pp; Japanese.
XX
XX A single-stranded DNA (or its complementary strand or the corresp. double
XX stranded DNA) which comprises one of the 7837 "GS" sequences given in
XX AAT19001-126837 and which is able to hybridise to part of human genomic
XX DNA, cDNA or mRNA is claimed. The GS (Gene Signature) sequences were
XX obtained from 3'-directed cDNA libraries prepared from various human
XX tissues; synthesis of cDNA was initiated from the 3'-end of mRNA by using
XX poly(T) as the sole primer. Since the 3'- untranslated sequence is unique
XX to a particular mRNA species, almost all the 3'-oriented cDNAs hybridise
XX with specific mRNAs. Each library is constructed so as to reflect
XX accurately the relative abundance of different mRNAs in the particular
XX tissue from which it was derived. The appearance frequency of a given GS
XX in a cDNA library can be determined (esp. using primers and probes
XX derived from the GS sequences) as a means of diagnosing abnormal cell
XX function or for recognising different cell types
XX
XX Sequence 78 BP; 30 A; 15 C; 12 G; 20 T; 0 U; 1 Other;
XX
XX Query Match 69.0%; Score 13.8; DB 2; Length 78;
XX Best Local Similarity 88.2%; Pred. No. 6.3e+03;
XX Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX 3 CCCATATTATGGAATG 19
XX | | | | | | | | | |
XX 33 CTCACATTATGGAATG 49
XX
XX RESULT 18
XX ABX67784/C
XX ID ABX67784 standard; DNA; 30 BP.
XX
XX AC ABX67784;
XX
XX 07-MAY-2003 (first entry)
XX
XX Novel Helicobacter pylori gene PCR primer #755.
XX
XX Protein-protein interaction; ulcer; selected interacting domain; SID;
XX PCR; primer; ss.
XX
XX Helicobacter pylori.
XX
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XX
XX M020026501-A2.
XX
XX 29-AUG-2002.
XX
XX 28-DEC-2001; 2001MO-EP015428.
XX
XX 02-JAN-2001; 2001US-0259302P.
XX
XX (HYBR-) HYBRIGENICS.
XX (INSP) INST PASTEUR.
XX
XX Legrain P, Rain J, Colland F, De Reuse H, Labigne A;
XX
XX WPI; 2002-674910/72.
XX
XX New complexes of protein-protein interactions in Helicobacter pylori,
XX useful for identifying modulating compounds for treating or preventing
XX ulcers in mammals.
XX
XX Example 9; Page 511; 642pp; English.
XX
XX The invention describes a complex of protein-protein interactions in
XX Helicobacter pylori selected from 421 complexes given in the
XX specification. The complex of protein-protein interactions are useful for
XX screening for agents which modulate the interaction of proteins.
XX Modulating compounds which binds to a targeted bacterial protein may be
XX used for treating or preventing ulcers in a human or animal. This
XX sequence represents a primer used to isolate polynucleotides encoding
XX Helicobacter pylori proteins for studies on protein-protein interactions
XX
XX Sequence 30 BP; 14 A; 5 C; 3 G; 5 T; 3 U; 0 Other;
XX
XX Query Match 68.0%; Score 13.6; DB 6; Length 30;
XX Best Local Similarity 80.0%; Pred. No. 7.4e+03;
XX Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
XX
XX 1 TCCCCATTTATGGAATGA 20
XX | | | | | | | | | |
XX 25 TCACCTTATTCATGGAATGA 6
XX
XX RESULT 19
XX ABZ50651
XX ID ABZ50651 standard; DNA; 41 BP.
XX
XX AC ABZ50651;
XX
XX 26-JUN-2003 (first entry)
XX
XX Human carboxyl ester lipase CEL gene polymorphic site, #7433.
XX
XX Human; drug metabolising enzyme; gene; drug metabolism; polymorphic site;
XX drug evaluation; drug screening; genotyping; genetic profiling;
XX therapeutic customisation; adverse reaction; clinical trial;
XX drug approval; single nucleotide polymorphism; SNP; ds.
XX
XX Homo sapiens.
XX
XX Key location/Qualifiers
XX variation replace(21,C)
XX FT /*tag= a
XX FT /standard_name= "Single nucleotide polymorphism (SNP)"
XX
XX M0200252044-A2.
XX
XX 04-JUL-2002.
XX
XX 27-DEC-2001; 2001WO-JP011592.
XX
XX 27-DEC-2000; 2000JP-00399443.
XX
XX 02-MAY-2001; 2001JP-00135256.
XX
XX 27-AUG-2001; 2001JP-00256862.
XX
```

QY 3 CCATATTATGGAATG 19
|||
DB 17 CCAACATTATGGAATG 1

RESULT 15

AD04818/C
ID AAD04818 standard; DNA, 23 BP.

AC AAD04818;

DT 17-JUL-2001 (first entry)

DE Human leptin receptor gene exon 6 forward (13F) RT-PCR primer.

XX Human; leptin receptor; anorectic; anabolic; fertility; energy balance;
KM thermoregulation; puberty; immunomodulatory; appetite; angiogenesis;
KW immunity; RT-PCR primer; ss.

OS Homo sapiens.

PN WO200130963-A2.

PD 03-MAY-2001.

PF 23-OCT-2000; 2000MO-11.000674.

PR 29-OCT-1999; 99US-0162220P.

PA (AGRI-) AGRIC RES ORG VOLCANI CENT.

PI Binat-Friedman M, Horev G, Eshdat Y;

DR WPI; 2001-308624/32.

PT New polynucleotide encoding avian lectin receptor, for e.g. identifying
modulators for controlling appetite and energy balance in poultry.

PS Example; Page 21; 67pp; English.

XX The present DNA sequence is human leptin receptor gene exon 6 forward
CC (13F) RT (Reverse Transcriptase)-PCR primer. This primer is used for
CC amplifying human leptin receptor gene by RT-PCR from human abdominal fat
CC mRNA, which is used for screening an adipose tissue-derived chicken cDNA
CC library. The invention relates to chicken leptin receptor and its
CC corresponding DNA molecule. Leptin receptor is used for regulating
CC appetite and other aspects of energy balance in poultry such as food
CC consumption, fat deposition, puberty, thermoregulation, immunity,
CC angiogenesis and energy expenditure. Leptin receptor is specifically used
CC for attenuating leptin activity in vivo (particularly using a soluble
CC form of the receptor, optionally expressed from a transgene). Leptin
CC receptor provides a replacement for the forced molting procedure to
CC improve performance and profitability of old laying hens. The invention
CC provides an assay for screening leptin agonists and antagonists. The
CC invention is also used to isolate leptin gene and to establish a bioassay
CC for leptin activity, e.g. to screen for birds with high or low leptin
CC levels in the blood (e.g. for breeding purposes) and/or for isolation of
CC mutated genes

XX Sequence 23 BP; 7 A; 5 C; 5 G; 6 T; 0 U; 0 Other;

QY Query Match 69.0%; Score 13.8; DB 4; Length 23;

Best Local Similarity 88.2%; Pred. No. 5.8e+03;

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 CCATATTATGGAATGA 20
|||||

DB 23 CCATATTATGGGCTGA 7

RESULT 16

ACI04232/C

ID ACI04232 standard; DNA; 25 BP.

XX ACI04232;

XX 13-OCT-2003 (first entry)

DE Human microarray DNA oligonucleotide SEQ ID NO 4223.

XX EST; ss; probe; expressed sequence tag; microarray; gene expression;
KM genetic variation; diallelic marker; polymorphism; human;
KW cross-species comparison.

OS Homo sapiens.

PN US2003104410-A1.

PD 05-JUN-2003.

PF 15-MAR-2002; 2002US-00098263.

PR 16-MAR-2001; 2001US-0276759P.

PA (AFPV-) AFFYMETRIX INC.

PI Miltmann MP;

DR WPI; 2003-567953/53.

PT New array of nucleic acid probes, useful for in situ hybridization, in
PT Southern, Northern or dot-blot hybridization to identify or detect the
PT sequence or specific mutations of any gene.

PS Claim 1; SEQ ID NO 4223; 9pp; English.

XX The invention discloses a microarray comprising a plurality of nucleic
CC acid probes including one of 2,018,500 fully defined sequences, or its
CC perfect match, perfect mismatch, antisense match or antisense mismatch.
CC Also disclosed is a method of gene expression analysis. The array is used
CC in monitoring gene expression levels by hybridisation to a DNA library,
CC in analysis of genetic variation or in hybridisation of tag-labelled
CC compounds. The nucleic acid probes are specifically designed for analysis
CC of at least one target sequence. The method of analysis comprises
CC hybridising at least one or more nucleic acids to at least two or more
CC nucleic acid probes and detecting the hybridisation. The nucleic acid
CC probes are attached to a solid support. The analysis comprises monitoring
CC gene expression levels, identifying diallelic markers or polymorphisms,
CC or family members of a gene and a cross-species comparison. Each of the
CC nucleic acids further comprises a tag sequence. The array of nucleic acid
CC probes is useful in in situ hybridisation, in Southern, Northern or dot-
CC blot hybridisation to identify or detect the sequence or specific
CC mutations of any gene, in mapping the 5' termini of mRNA molecules by
CC primer extensions or in screening cDNA or genomic libraries or subclones
CC for additional subclones containing segments of DNA that have been
CC isolated and previously sequenced. The sequence presented is one of the
CC nucleic acid probes incorporated in the microarray. Note: The sequence
CC data for this patent can also be obtained in electronic format directly
CC from USPTO at seqdata.uspto.gov/sequence.html

XX Sequence 25 BP; 6 A; 6 C; 4 G; 9 T; 0 U; 0 Other;

QY Query Match 69.0%; Score 13.8; DB 9; Length 25;

Best Local Similarity 88.2%; Pred. No. 5.8e+03;

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 CCATATTATGGAATGA 20
|||||

DB 25 CCATGTTTACGGAATGA 9

RESULT 17

AAT19807

ID AAT19807 standard; cDNA to mRNA; 78 BP.

XX

OS Homo sapiens.
XX WO2004076639-A2.
PN 10-SEP-2004.
XX 26-FEB-2004; 2004WO-US005655.
PF 26-FEB-2003; 2003US-0449693P.
XX 26-FEB-2003; 2003US-0449753P.
PR 26-FEB-2003; 2003US-0449753P.
XX 26-FEB-2003; 2003US-0449795P.
XX (AMHP) WYETH.
PA (OTOO/) O'TOOLE M M.
XX (WEIL/) WEI L.
PI O'toole MM, Wei L;
XX WPI; 2004-662008/64.
DR WPI; 2004-662008/64.
XX
XX New pharmaceutical composition comprising a polypeptide encoded by a gene
PT that is differentially expressed in a pre-symptomatic lupus-affected or -
PT prediposed tissues, and a carrier, useful for treating lupus.
XX
XX Claim 17; SEQ ID NO 7426; 86bp; English.
PS
XX The invention relates to a pharmaceutical composition comprising a
CC carrier and at least one active component selected from a polypeptide
CC encoded by a gene that is differentially expressed in pre-symptomatic
CC lupus-affected or lupus-prediposed tissues as compared to disease-free
CC tissues, a variant of the polypeptide and a polynucleotide encoding the
CC polypeptide or variant. The invention also relates to detecting an
CC expression profile of at least one gene in a biological sample of a
CC subject and comparing the expression profile to a reference expression
CC profile of the gene to detect or monitor an autoimmune disease in a
CC subject, where the gene is differentially expressed in pre-symptomatic
CC lupus-affected or lupus-prediposed tissues as compared to disease-free
CC tissues, administering a therapeutically or prophylactically effective
CC amount of the pharmaceutical composition in a subject, preferably a human
CC who has or is prediposed to systemic lupus erythematosus or lupus
CC nephritis, contacting an agent with lupus-affected or lupus-prediposed
CC cells and comparing expression profiles or protein activities of at least
CC one gene in the cells before and after the contacting to determine if the
CC agent modulates expression or protein activity of at least one gene,
CC administering an agent to a lupus-affected or lupus-prediposed subject
CC and comparing expression profiles or protein activities of at least one
CC gene in the biological sample before and after the administering to
CC determine if the agent modulates expression or protein activity of at
CC least one gene in the subject, where the gene is differentially expressed
CC in lupus-affected or lupus-prediposed kidney tissues as compared to
CC disease-free kidney tissues. The pharmaceutical composition is useful for
CC diagnosing, treating and preventing autoimmune diseases such as lupus
CC nephritis and systemic lupus erythematosus. This sequence represents a
CC human lupus-related siRNA target sequence of the invention. Note: The
CC sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 21 BP; 6 A; 4 C; 4 G; 7 T; 0 U; 0 Other;
Query Match 69.0%; Score 13.8; DB 13; Length 21;
Best Local Similarity 88.2%; Pred. No. 5.7e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 3 CCATATTATGATGATG 19
DB 17 CCAACATTATGATGATG 1

AC AEA84363;
XX
XX 11-AUG-2005 (first entry)
DT
XX Human lupus-related siRNA target sequence #3207.
DE
XX
XX
XX Diagnosis; genetic marker; autoimmune disease;
KM systemic lupus erythematosus; lupus nephritis;
KM immunosuppressive; nephrotropic; antiinflammatory; dermatological; ss.
XX
XX Homo sapiens.
OS
XX WO2004076639-A2.
PN 10-SEP-2004.
XX 26-FEB-2004; 2004WO-US005655.
PF 26-FEB-2003; 2003US-0449693P.
XX 26-FEB-2003; 2003US-0449753P.
PR 26-FEB-2003; 2003US-0449753P.
XX 26-FEB-2003; 2003US-0449795P.
XX (AMHP) WYETH.
PA (OTOO/) O'TOOLE M M.
XX (WEIL/) WEI L.
PI O'toole MM, Wei L;
XX WPI; 2004-662008/64.
DR WPI; 2004-662008/64.
XX
XX New pharmaceutical composition comprising a polypeptide encoded by a gene
PT that is differentially expressed in a pre-symptomatic lupus-affected or -
PT prediposed tissues, and a carrier, useful for treating lupus.
XX
XX Claim 17; SEQ ID NO 9676; 86bp; English.
PS
XX The invention relates to a pharmaceutical composition comprising a
CC carrier and at least one active component selected from a polypeptide
CC encoded by a gene that is differentially expressed in pre-symptomatic
CC lupus-affected or lupus-prediposed tissues as compared to disease-free
CC tissues, a variant of the polypeptide and a polynucleotide encoding the
CC polypeptide or variant. The invention also relates to detecting an
CC expression profile of at least one gene in a biological sample of a
CC subject and comparing the expression profile to a reference expression
CC profile of the gene to detect or monitor an autoimmune disease in a
CC subject, where the gene is differentially expressed in pre-symptomatic
CC lupus-affected or lupus-prediposed tissues as compared to disease-free
CC tissues, administering a therapeutically or prophylactically effective
CC amount of the pharmaceutical composition in a subject, preferably a human
CC who has or is prediposed to systemic lupus erythematosus or lupus
CC nephritis, contacting an agent with lupus-affected or lupus-prediposed
CC cells and comparing expression profiles or protein activities of at least
CC one gene in the cells before and after the contacting to determine if the
CC agent modulates expression or protein activity of at least one gene,
CC administering an agent to a lupus-affected or lupus-prediposed subject
CC and comparing expression profiles or protein activities of at least one
CC gene in the biological sample before and after the administering to
CC determine if the agent modulates expression or protein activity of at
CC least one gene in the subject, where the gene is differentially expressed
CC in lupus-affected or lupus-prediposed kidney tissues as compared to
CC disease-free kidney tissues. The pharmaceutical composition is useful for
CC diagnosing, treating and preventing autoimmune diseases such as lupus
CC nephritis and systemic lupus erythematosus. This sequence represents a
CC human lupus-related siRNA target sequence of the invention. Note: The
CC sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 21 BP; 6 A; 4 C; 4 G; 7 T; 0 U; 0 Other;
Query Match 69.0%; Score 13.8; DB 13; Length 21;
Best Local Similarity 88.2%; Pred. No. 5.7e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TCCCATATTGATGA 16
DB 1 TCCCATATTGATGA 16

RESULT 11
ID ADY74704/c
ADY74704 standard; DNA; 25 BP.

AC ADY74704;
XX
XX 02-JUN-2005 (first entry)

DE Receptor activator of NF-kappaB ligand (RANKL) 5' PCR primer Seq 349.
XX Receptor activator of NF-kappaB ligand; RANKL; animal disease model;
KM metabolic bone disease; screening; osteopathic; osteoporosis;
KM antisense therapy; PCR; primer; ss.

OS Synthetic.

PN US2005060764-A1.

XX 17-MAR-2005.

XX 17-SEP-2003; 2003US-00667236.

XX 17-SEP-2003; 2003US-00667236.

PA (GREG/) GREGORY S.

PI Gregory S;

XX WPI; 2005-222272/23.

PT New mouse model exposed to parathyroid hormone (PTH), its analog or
PT fragment so that serum calcium concentration and RANKL mRNA expression
PT are increased, useful for screening agents for treating or preventing
PT osteoporosis.

XX Example 23; SEQ ID NO 349; 101pp; English.

XX This invention relates to novel mouse model for bone metabolism.
XX Specifically, it refers to a mouse that is exposed to a compound selected
XX from parathyroid hormone (PTH), its analogue or a fragment thereof, for a
XX time sufficient to allow serum calcium concentration and the receptor
XX activator of Nkrpab ligand (RANKL) mRNA expression to increase in the
XX mouse model. Note that the RANKL gene maps to human chromosome 13q14 and
XX is also known as tumor necrosis factor (TNF)-related activator-induced
XX cytokine (TRANCE), osteoprotegerin ligand (OPGL), osteoclast
XX differentiation factor (ODF) and TNFSF11. The present invention describes
XX a screening method to identify potential therapeutic agents with
XX osteopathic activity that can affect bone metabolism and are useful for
XX the treatment or prevention of osteoporosis. As such, it refers to
XX administering this agent to the mouse model and assessing the mouse for
XX an alteration in a bone metabolism related marker such as RANKL.
XX Furthermore, it describes a method for testing a mouse model for bone
XX metabolism disease by administering an antisense oligonucleotide to
XX modulate RANKL or RANKL mRNA expression, and subsequently administering
XX PTH to the mouse in order to assess the effect of the antisense oligo on
XX the mouse compared to a control mouse treated with calcitonin. This
XX oligonucleotide sequence is a PCR primer given in an exemplification of
XX the invention.

XX Sequence 25 BP; 6 A; 2 C; 6 G; 11 T; 0 U; 0 Other;

QY Query Match 71.0%; Score 14.2; DB 14; Length 25;
Best Local Similarity 84.2%; Pred. No. 3.7e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 CCCCATATTGATGA 20
DB 20 CCCCATATTGATGA 20

RESULT 12
ID ADY97749/c
ADY97749 standard; DNA; 25 BP.

AC ADY97749;
XX
XX 16-JUN-2005 (first entry)

DE Mouse RANKL forward PCR primer SEQ ID NO 349.

XX RANKL; osteoporosis; multiple myeloma; rheumatoid arthritis; cytostatic;
KM osteopathic; antiarthritic; antirheumatic; antisense therapy;
KM hematological disease; immune disorder; degeneration; endocrine disease;
KM musculoskeletal disease; inflammation; ss; PCR; primer.

XX Mus sp.

PN WO2005028633-A2.

XX 31-MAR-2005.

XX 17-SEP-2004; 2004WO-US030736.

XX 17-SEP-2003; 2003US-0560750P.

PA (ISIS-) ISIS PHARM INC.

PI Baker BF, Bennett FC, Dobie KW, Myers K, Finger J, Cowseart IM;

XX WPI; 2005-254125/26.

PT New compound comprising 8 to 80 nucleobases targeted to a nucleic acid
PT molecule encoding RANKL, useful in preparing a composition for treating
PT or preventing a RANKL associated conditions e.g. osteoporosis.

XX Example 23; SEQ ID NO 349; 259pp; English.

XX The invention relates to a compound targeted to a nucleic acid molecule
XX encoding RANKL which inhibits the expression of RANKL mRNA by at least
XX 10%. The compound is useful in preparing a composition for treating or
XX preventing a RANKL associated disease or condition in an animal, e.g.,
XX bone metabolism disease, osteoporosis, multiple myeloma, breast cancer
XX related osteolysis, rheumatoid arthritis, collagen-induced arthritis or
XX CC adjuvant-induced arthritis. The present sequence represents a mouse RANKL
XX PCR primer.

XX Sequence 25 BP; 6 A; 2 C; 6 G; 11 T; 0 U; 0 Other;

QY Query Match 71.0%; Score 14.2; DB 14; Length 25;
Best Local Similarity 84.2%; Pred. No. 3.7e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 CCCCATATTGATGA 20
DB 20 CCCCATATTGATGA 20

RESULT 13
ID AEA82113/c
AEA82113 standard; cDNA; 21 BP.

XX AEA82113;

XX 11-AUG-2005 (first entry)

DE Human lupus-related siRNA target sequence #2457.

XX diagnosis; genetic marker; autoimmune disease;
KM systemic lupus erythematosus; lupus nephritis; nephritis;
KM immunosuppressive; nephrotropic; antiinflammatory; dermatological; ss.

XX	Rat superoxide dismutase 1 gene antisense oligo #110.
DE	
XX	antimicrobial; antiinflammatory; cyostatic; antisense therapy;
KM	superoxide dismutase; superoxide dismutase modulator; infection;
KW	inflammation; tumor; ss; gene expression; 2'-MOE; 2'-MOE wings;
KX	2'-methoxyethyl; phosphorothioate.
OS	Rattus norvegicus.
OS	Synthetic.
XH	
XX	
FH	Key Location/Qualifiers
FT	modified_base 1..20
FT	/tag= b
FT	/mod_base= OTHER
FT	/note= "all internucleotide linkages are phosphorothioate
FT	linkages. All C bases are 5-methylcytidine bases"
FT	modified_base 1..5
FT	/tag= a
FT	/mod_base= OTHER
FT	/note= "2'-methoxyethyl nucleotides"
FT	modified_base 16..20
FT	/tag= c
FT	/mod_base= OTHER
FT	/note= "2'-methoxyethyl nucleotides"
XX	
XX	US2005019915-A1.
PN	
PD	27-JAN-2005.
PF	26-SEP-2003; 2003US-00672866.
PR	21-JUN-2001; 2001US-00888360.
PR	04-AUG-2003; 2003US-00633843.
XX	
PA	(BENNETT) BENNETT C F.
PA	(DOBIE) DOBIE K W.
PB	Bennett CF, Dobie KW;
PI	
XX	WPI; 2005-100832/11.
DR	
XX	
PT	New antisense compound which specifically hybridizes with and inhibits
PT	the expression of human superoxide dismutase 1, soluble, useful for
PT	treating diseases associated with expression of superoxide dismutase 1,
PT	soluble.
XX	
PS	Example 19; SEQ ID NO 271; 116pp; English.
XX	
CC	The invention relates to an antisense compound 8-50 nucleobases in length
CC	targeted to nucleobases 96-523 of a coding region of a nucleic acid
CC	molecule encoding human superoxide dismutase 1, soluble comprising 874 bp
CC	fully defined in the specification, where the compound specifically
CC	hybridizes with and inhibits the expression of human superoxide dismutase
CC	1, soluble. The compound is useful for modulating of superoxide dismutase
CC	1, soluble expression or for treating diseases associated with expression
CC	of superoxide dismutase 1, soluble. It can also be used to prevent or
CC	delay infection, inflammation, or tumor formation. This sequence
CC	corresponds to an antisense oligonucleotide targeted to the rat
CC	superoxide dismutase 1 gene for inhibition of gene expression.
XX	
SO	Sequence 20 BP; 5 A; 4 C; 4 G; 7 T; 0 U; 0 Other;
QY	Query Match 72.0%; Score 14.4; DB 14; Length 20;
DB	Best Local Similarity 93.8%; Pred. No. 2.9e+03;
	Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0
	1 TCCCCATATTATGGA 16
	5 TCCCATAATTGATGGA 20
RESULT	10

ADW64179	ID	ADW64179 standard; DNA; 20 BP.
XX	XX	
XX	ADW64179;	
AC	DT	07-APR-2005 (first entry)
XX	XX	
DE	Rat superoxide dismutase 1 gene antisense oligo #108.	
XX	XX	
KM	antimicrobial; antiinflammatory; cytosratic; antisense therapy;	
KM	superoxide dismutase; superoxide dismutase modulator; infection;	
KM	inflammation; tumor; ss; gene expression; 2'-MOE; 2'-MOE wings;	
XX	2'-methoxyethyl; phosphorothioate.	
OS	Rattus norvegicus.	
OS	Synthetic.	
FX	Key	Location/Qualifiers
FH	modified_base	1..20
FT	/+cag= b	
FT	/mod_base= OTHER	
FT	/note= "all internucleotide linkages are phosphorothioate	
FT	linkages. All C bases are 5-methylcyridine bases"	
FT	modified_base	1..5
FT	/+cag= a	
FT	/mod_base= OTHER	
FT	/note= "2'-methoxyethyl nucleotides"	
FT	modified_base	16..20
FT	/+cag= c	
FT	/mod_base= OTHER	
FT	/note= "2'-methoxyethyl nucleotides"	
XX	US2005019915-A1.	
PN	27-JAN-2005.	
XX	XX	
PD	26-SEP-2003; 2003US-00672866.	
XX	XX	
PF	21-JUN-2001; 2001US-00888360.	
XX	XX	
PR	04-AUG-2003; 2003US-00633843.	
PA	(BENNY) BENNETT C F.	
PA	(DOBI/) DOBIE K W.	
PI	Bennett CF, Dobie KW;	
XX	WP1; 2005-100832/11.	
XX	XX	
XX	New antisense compound which specifically hybridizes with and inhibits	
PT	the expression of human superoxide dismutase 1, soluble, useful for	
PT	treating diseases associated with expression of superoxide dismutase 1,	
PT	soluble.	
XX	XX	
PS	Example 19; SEQ ID NO 269; 116pp; English.	
XX	XX	
CC	The invention relates to an antisense compound 8-50 nucleobases in length	
CC	targeted to nucleobases 96-523 of a coding region of a nucleic acid	
CC	molecule encoding human superoxide dismutase 1, soluble comprising 874 bp	
CC	fully defined in the specification, where the compound specifically	
CC	hybridizes with and inhibits the expression of human superoxide dismutase	
CC	1, soluble. The compound is useful for modulating of superoxide dismutase	
CC	1, soluble expression or for treating diseases associated with expression	
CC	of superoxide dismutase 1, soluble. It can also be used to prevent or	
CC	delay infection, inflammation, or tumor formation. This sequence	
CC	corresponds to an antisense oligonucleotide targeted to the rat	
CC	superoxide dismutase 1 gene for inhibition of gene expression.	
XX	Sequence 20 BP; 5 A; 5 C; 4 G; 6 T; 0 U; 0 Other;	
SQ	Query Match	72.0%; Score 14.4; DB 14; Length 20;
	Best Local Similarity	93.8%; Pred. No.2.9e+03;
	Matches 15; Conservative	0; Mismatches 1; Indels 0; Gaps 0

XX Human silent SNP containing nucleic acid SEQ:5711.
DE
XX
KW Human; single nucleotide polymorphism; SNP; genome; gene therapy;
KW protein therapy; vaccine; probe; diagnostic assay; detection;
KW quantitation; restorative therapy; polymorphic; ds.
XX
OS Homo sapiens.
XX
PN WO200140521-A2.
XX
PD 07-JUN-2001.
XX
PF 30-NOV-2000; 2000WO-US032758.
XX
PR 30-NOV-1999; 99US-0168138P.
PR 29-NOV-2000; 2000US-00726173.
XX
XX (CURA-) CURAGEN CORP.
XX
XX Shimkets RA, Leach M;
PI
DR WPI; 2001-356160/37.
XX
PT Polymorphic nucleic acid sequences, useful in genetic testing and
PT therapy.
XX
PS Claim 1; Page 2258; 2653pp; English.
XX
CC AA173060 to AA179867 represent isolated human polymorphic polynucleotide
CC sequences (I), which contain single nucleotide polymorphisms (SNPs).
CC AAM53114 to AAM53329 represent peptides related to human polymorphic
CC polynucleotide sequences. The sequences can be used in gene and protein
CC therapy, and in vaccine production. (I) and the polypeptides encoded by
CC them may be used in the prevention, diagnosis and treatment of diseases
CC associated with inappropriate expression of polymorphic polypeptides. For
CC example, (I) may be used to treat disorders by rectifying mutations or
CC deletions in a patient's genome that affect the activity of polypeptides
CC by expressing inactive proteins or to supplement the patients own
CC production of polypeptide. Additionally, (I) and its complementary
CC sequences may also be used as DNA probes in diagnostic assays to detect
CC and quantitate the presence of similar nucleic acids in samples, and
CC therefore which patients may be in need of restorative therapy. The
CC polypeptides encoded by (I) may be used as antigens in the production of
CC antibodies specific for polymorphic polypeptides. The antibodies may also
CC be used to down regulate expression and activity. The antibodies may also
CC be used as diagnostic agents for detecting the presence of polymorphic
CC polypeptides in samples
XX
SQ Sequence 51 BP; 25 A; 7 C; 7 G; 12 T; 0 U; 0 Other;
XX
Query Match 75.0%; Score 15; DB 4; Length 51;
Best Local Similarity 100.0%; Pred.No.1.6e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 6 ATATTATGGAATGA 20
Db 27 ATATTATGGAATGA 13
XX
RESULT 8
ADW64180
ID ADW64180 standard; DNA; 20 BP.
XX
AC ADW64180;
XX
DT 07-APR-2005 (first entry)
XX
DE Rat superoxide dismutase 1 gene antisense oligo #109.
XX
KW antimicrobial; antiinflammatory; cytostatic; antisense therapy;
KW superoxide dismutase; superoxide dismutase modulator; infection;
KW inflammation; tumor; ss; gene expression; 2'-MOE; 2'-MOE wings;

KW 2'-methoxyethyl; phosphorothioate.
XX
XX Rattus norvegicus.
OS Synthetic.
XX
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= b
FT /mod_base= OTHER
FT /note= "all internucleotide linkages are phosphorothioate
FT linkages. All C bases are 5-methylcytidine bases"
FT modified_base 1..5
FT /*tag= a
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl nucleotides"
FT modified_base 15..20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl nucleotides"
XX
PN US2005019915-A1.
XX
PD 27-JAN-2005.
XX
PF 26-SBP-2003; 2003US-00672866.
XX
PR 21-JUN-2001; 2001US-00888360.
PR 04-AUG-2003; 2003US-00633843.
XX
XX (BENN/) BENNETT C F.
PA (DOB/) DOBLE K W.
PI Bennett CF, Doble KW;
XX
DR WPI; 2005-100832/11.
XX
XX New antisense compound which specifically hybridizes with and inhibits
PT the expression of human superoxide dismutase 1, soluble, useful for
PT treating diseases associated with expression of superoxide dismutase 1,
PT soluble.
XX
XX Example 19; SEQ ID NO 270; 116pp; English.
PS
XX The invention relates to an antisense compound 8-50 nucleobases in length
XX targeted to nucleobases 96-523 of a coding region of a nucleic acid
CC molecule encoding human superoxide dismutase 1, soluble comprising 874 bp
CC fully defined in the specification, where the compound specifically
CC hybridizes with and inhibits the expression of human superoxide dismutase
CC 1, soluble. The compound is useful for modulating of superoxide dismutase
CC 1, soluble expression or for treating diseases associated with expression
CC of superoxide dismutase 1, soluble. It can also be used to prevent or
CC delay infection, inflammation, or tumor formation. This sequence
CC corresponds to an antisense oligonucleotide targeted to the rat
CC superoxide dismutase 1 gene for inhibition of gene expression.
XX
SQ Sequence 20 BP; 5 A; 5 C; 4 G; 6 T; 0 U; 0 Other;
XX
Query Match 72.0%; Score 14.4; DB 14; Length 20;
Best Local Similarity 93.8%; Pred.No.2.9e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 TCCCATATTGATGA 16
Db 3 TCCCATATTGATGA 18
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XX
AC ADW64181;
XX
DT 07-APR-2005 (first entry)

PD	27-FEB-2003.
XX	
PF	16-AUG-2002; 2002WO-US026514.
XX	
PR	16-AUG-2001; 2001US-0313080P.
XX	
PA	(PHAS-) PHASE-I MOLECULAR TOXICOLOGY INC.
P1	Neft RE, Dunn RT, Adkins K, Pickett GS, Kier LD, Schweizer K;
P1	Alen P;
DR	WPI; 2003-266322/26.
XX	
XX	
PS	Claim 1; Page 342; 455pp; English.
XX	
CC	The present invention describes a method (M1) for determining a
CC	toxicological response to an agent, which comprises comparing the
CC	expression profile of one or more human toxic response genes to a
CC	reference gene expression profile indicative of toxicity, and so
CC	determining the presence of a toxic response to the agent. Also
CC	described: (1) an array comprising one or more polynucleotides selected
CC	from the genes corresponding to the partial sequences given in ABZ82842
CC	to ABZ84764, or their fragments of at least 20 nucleotides, or homologues
CC	; and (2) determining if a gene putatively identified to be a toxic
CC	response gene plays a role on toxic response pathways by determining the
CC	expression profile of the gene after exposure of cells or a human subject
CC	to a known toxic pharmaceutical or industrial agent, comprising: (a)
CC	exposing cells to an agent or isolating cells from a human subject who
CC	was exposed to an agent; (b) obtaining the test gene expression profile
CC	for a putatively identified toxic response gene after exposure to a known
CC	toxic pharmaceutical or industrial agent; and (c) comparing the test
CC	profile to the expression profile of a gene with a similar function or
CC	comparing the test profile to the expression profile of that gene after
CC	exposure to other known toxic compounds. The methods are useful for
CC	predicting and determining toxicological responses on a cellular, organ
CC	or system level. The arrays comprising the human genes are useful for
CC	toxicological screening of drugs, pharmaceutical compounds and chemicals
XX	
SQ	Sequence 25 BP; 8 A; 3 C; 8 G; 6 T; 0 U; 0 Other;
Query Match	79.0%; Score 15.8; DB 10; Length 25;
Best Local Similarity	89.5%; Pred. No. 5.9e+02; Mismatches 2; Indels 0; Gaps 0
Matches	17; Conservative 0;
OY	2 CCCCATATTTATGCAATGA 20 Db 1 CCCCATATTTATGGAACGA 19
RESULT 6	
AEB27395/C	
ID	AEB27395 standard; DNA; 60 BP.
XX	
AC	AEB27395;
XX	
DT	22-SEP-2005 (first entry)
XX	
DE	P. radiata cell cycle gene microarray oligo SEQ ID NO 556.
XX	
KM	plant protectant; fungicide; plant growth regulant; gene therapy;
KW	cell cycle; gene expression; plant; transgenic plant; microarray; wood;
ss.	
OS	Pinus radiata.
XX	
PN	WO2005065339-A2.
XX	

XX	21-JUL-2005.
PD	
PR	30-DEC-2004; 2004WO-US043804.
XX	
PA	30-DEC-2003; 2003US-0533036P.
XX	
PA	(ARBO-) ARBOGEN LLC.
PA	(GENE-) GENESIS RES & DEV CORP LTD.
XX	
P1	Forster RL, Connett MB, Emerson SJ, Grigor MR, Higgins CM;
P1	Lund ST, Magnusin A, Kodrzycki RJ;
XX	
DR	WPI; 2005-506765/51.
XX	
PT	New polynucleotide encoding a plant cell cycle protein, useful for
PT	modifying plant development and altering plant phenotype.
PS	
XS	Claim 43; SEQ ID NO 556; 499pp; English.
CC	
CC	The invention describes an isolated polynucleotide comprising: (i) a
CC	sequence of SEQ ID NOS: 1-237 or their conservative variants; (ii) a
CC	sequence encoding the catalytic or substrate-binding domain of a
CC	polypeptide of SEQ ID NOS: 261-497, where the polynucleotide encodes a
CC	polypeptide having the activity of the polypeptide of SEQ ID NOS: 261-497
CC	; or (iii) a nucleic acid sequence of SEQ ID NOS: 471-697. Also described
CC	are: (1) a DNA construct comprising at least one polynucleotide having
CC	the sequence of SEQ ID NOS: 1-237 or their conservative variants; (2) a
CC	plant cell transformed with the DNA construct of (1); (3) a transgenic
CC	plant comprising the plant cell of (2); (4) a method of making a
CC	transformed plant; (5) a wood or a wood pulp obtained from a transgenic
CC	tree which has been transformed with the DNA construct of (1); (6) a
CC	method of making wood or wood pulp; (7) an isolated polypeptide
CC	comprising an amino acid sequence encoded by the new isolated
CC	polynucleotide or comprising any of the amino acid sequences of SEQ ID
CC	NOS: 261-497; (8) a method of altering a plant phenotype of a plant; (9)
CC	a method of correlating gene expression in two different samples; (10) a
CC	method of correlating the possession of a plant phenotype to the level of
CC	gene expression in the plant of one or more genes; (11) a method of
CC	correlating gene expression to a stage of the cell cycle; (12) a
CC	combination, for detecting expression of one or more genes, comprising
CC	two or more oligonucleotides, where each oligonucleotide is capable of
CC	hybridizing to a nucleic acid sequence of SEQ ID NOS: 1-237 or to gene
CC	a product encoded by a nucleic acid sequence of SEQ ID NOS: 1-237; (13) a
CC	microarray comprising the combination of (12) provided on a solid
CC	support, where each of the two or more oligonucleotides occupies a unique
CC	location on the solid support; (14) a method for detecting one or more
CC	genes in a sample; (15) a method for detecting one or more nucleic acid
CC	sequences encoded by one or more genes in a sample; and (16) a kit, for
CC	detecting gene expression, comprising the microarray of (13) together
CC	with one or more buffers or reagents for a nucleotide hybridization
CC	reaction. The polynucleotides, polypeptides, DNA construct, composition,
CC	and methods are useful for modifying plant development and altering plant
CC	phenotype. This sequence represents an oligonucleotide used in the
CC	creation of a microarray for detection of cell cycle genes.
SQ	
	Sequence 60 BP; 14 A; 12 C; 13 G; 21 T; 0 U; 0 Other:
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DB	53 TCCTCAAACTTATGGAAAGA 34
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ID	AAI78770 standard; DNA; 51 BP.
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AC	AAI78770;
XX	
DT	09-NOV-2001 (first entry)

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RESULT 3
ADN49091/c
ID ADN49091 standard; DNA; 20 BP.
XX
AC ADN49091;
XX
DT 15-JUL-2004 (first entry)
XX
DE Human histone deacetylase 2 (HDAC2) DNA target region #15.
XX
KM Histone deacetylase 2; HDAC2; HDAC-2; hdac2; RPD3; hRPD3;
KM hyperproliferative disorder; cancer; antisense gene therapy; human; ds;
KM chromosome 6q21.
XX
OS Homo sapiens.
XX
PN US2004077578-A1.
XX
PD 22-APR-2004.
XX
PF 02-SEP-2003; 2003US-00653528.
XX
PR 14-JUN-2002; 2002US-00173192.
XX
PA (MONI/) MONIA B P.
PA (DOBI/) DOBIE K W.
XX
PI Monia BP, Dobie KW;
XX
DR WPI; 2004-340037/31.
XX
PT New compound, having a sequence targeted to a coding region of a nucleic
PT acid encoding human histone deacetylase 2, useful for preparing a
PT composition for treating hyperproliferative disorders, e.g., cancer.
XX
PS Example 15; SEQ ID NO 62; 47bp; English.
XX
CC The invention relates to antisense compounds, compositions and methods
CC for modulating the expression of histone deacetylase 2 (HDAC2). HDAC2 is
CC also known as HDAC-2, hdac2, human RPD3 and hRPD3. The composition
CC comprises antisense compounds that can be targeted towards HDAC2. The
CC compound is useful for preparing a composition for treating
CC hyperproliferative disorders, e.g., cancer. It is also useful in
CC antisense gene therapy. The present sequence is human HDAC2 DNA target
CC region. Human HDAC2 gene is located at chromosome 6q21.
XX
SQ Sequence 20 BP; 7 A; 3 C; 4 G; 6 T; 0 U; 0 Other;
Query Match 100.0%; Score 20; DB 12; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.8;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 20 TCCCCATATTATGGAATGA 1
RESULT 4
ADN49066
ID ADN49066 standard; DNA; 20 BP.
XX
AC ADN49066;
XX
DT 15-JUL-2004 (first entry)
XX
DE Human HDAC2 specific antisense oligo, ISIS 157268.
XX
KM Histone deacetylase 2; HDAC2; HDAC-2; hdac2; RPD3; hRPD3;
KM hyperproliferative disorder; cancer; antisense gene therapy; human;
KM antisense; phosphorothioate backbone; ss.
XX
OS Homo sapiens.
OS Synthetic.
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XX
FH Key Location/Qualifiers
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FT /note="Phosphorothioate backbone in which all cytidines
FT are 5-methylcytidines"
FT 1..5
FT /*tag= a
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FT /note="2'-methoxyethyl bases"
FT 16..20
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PN US2004077578-A1.
XX
PD 22-APR-2004.
XX
PF 02-SEP-2003; 2003US-00653528.
XX
PR 14-JUN-2002; 2002US-00173192.
XX
PA (MONI/) MONIA B P.
PA (DOBI/) DOBIE K W.
XX
PI Monia BP, Dobie KW;
XX
DR WPI; 2004-340037/31.
XX
PT New compound, having a sequence targeted to a coding region of a nucleic
PT acid encoding human histone deacetylase 2, useful for preparing a
PT composition for treating hyperproliferative disorders, e.g., cancer.
XX
PS Example 15; SEQ ID NO 37; 47bp; English.
XX
CC The invention relates to antisense compounds, compositions and methods
CC for modulating the expression of histone deacetylase 2 (HDAC2). HDAC2 is
CC also known as HDAC-2, hdac2, human RPD3 and hRPD3. The composition
CC comprises antisense compounds that can be targeted towards HDAC2. The
CC compound is useful for preparing a composition for treating
CC hyperproliferative disorders, e.g., cancer. It is also useful in
CC antisense gene therapy. The present sequence is an antisense
CC oligonucleotide targeted to human HDAC2 DNA.
XX
SQ Sequence 20 BP; 6 A; 4 C; 3 G; 7 T; 0 U; 0 Other;
Query Match 100.0%; Score 20; DB 12; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.8;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TCCCCATATTATGGAATGA 20
DB 1 TCCCCATATTATGGAATGA 20
RESULT 5
ABZ84349
ID ABZ84349 standard; DNA; 25 BP.
XX
AC ABZ84349;
XX
DT 14-MAY-2003 (first entry)
XX
DE Toxicologically relevant human PCR primer #1508.
XX
KM Toxicologically relevant gene; toxicological response; PCR primer; ss.
XX
OS Homo sapiens.
OS Synthetic.
PN WO2003016500-A2.
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GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: March 1, 2006, 22:25:00 ; Search time 336.667 Seconds
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Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 5180220

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Post-processing: Minimum Match 0%
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Listing first 100 summaries

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13: geneseq2005s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

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2	20	100.0	20	12	ADJ27020 Human his
3	20	100.0	20	12	ADN49091 Human his
4	20	100.0	20	12	ADN49066 Human HDA
5	15.8	79.0	25	10	ABZ84349 Toxicolog
6	15.2	76.0	25	14	ABE87395 P. radiat
7	15	75.0	51	4	AAI78770 Human sil
8	14.4	72.0	20	14	ADM64180 Rat super
9	14.4	72.0	20	14	ADM64181 Rat super
10	14.4	72.0	20	14	ADM64179 Rat super
11	14.2	71.0	25	14	ADY74704 Receptor
12	14.2	71.0	25	14	ADY7749 Mouse RAN
13	13.8	69.0	21	13	AEA82113 Human lyp
14	13.8	69.0	21	13	AEA84363 Human lyp
15	13.8	69.0	23	4	AAD04818 Human lep
16	13.8	69.0	25	9	ACT04232 Human mic
17	13.8	69.0	78	2	AAI19807 Human gen
18	13.6	68.0	30	6	ABX67784 Novel Hel
19	13.6	68.0	41	6	ABZ50651 Human car

20	13.6	68.0	47	3	AAZ66376 Human map
21	13.6	68.0	50	13	ADS92006 DNA oligo
22	13.6	68.0	60	13	ADSS3601 Escalypu
23	13.6	68.0	65	6	ABN54206 Mouse spl
24	13.4	67.0	19	10	ADJ66231 Human TGF
25	13.4	67.0	19	10	ADJ66359 Human TGF
26	13.4	67.0	26	14	ADW81692 MAP3K9 ma
27	13.4	67.0	51	4	AAI78771 Human sil
28	13.4	67.0	71	8	ABX50279 Bovine ES
29	13.2	66.0	20	5	AAH20687 Human tel
30	13.2	66.0	20	12	ADJ54571 Human B7-
31	13.2	66.0	20	13	ADU91691 Human B7-
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33	13.2	66.0	20	14	ADM50368 Human B7-
34	13.2	66.0	20	14	ADM50252 Human B7-
35	13.2	66.0	21	14	ADM84597 MAP3K9 ma
36	13.2	66.0	25	9	ACK21086 Human mic
37	13.2	66.0	25	13	ADJ54571 Human B7-
38	13.2	66.0	26	2	AAQ41629 TGF-beta2
39	13.2	66.0	26	2	AAQ41628 TGF-beta2
40	13.2	66.0	26	5	AAI62396 Soybean 5
41	13.2	66.0	29	8	ACC79435 CFA/I det
42	13.2	66.0	30	3	AAZ25395 Maize sta
43	13.2	66.0	30	3	ABX68831 Novel Hel
44	13.2	66.0	35	13	ADU46633 PCR prime
45	13.2	66.0	38	4	AAAC6288 PCR prime
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49	13.2	66.0	41	14	AEA64396 Oligonuc
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51	13.2	66.0	45	2	AAV50372 PCR prime
52	13.2	66.0	45	6	ABK48027 Human Cdk
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64	12.8	64.0	20	10	ABZ85577 Human oii
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72	12.8	64.0	25	13	ADJ15521 Mouse flo
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74	12.8	64.0	31	2	AAAT1294 Guy's 13
75	12.8	64.0	31	2	AAAT97888 Hybrid Gu
76	12.8	64.0	32	6	ABN83994 Bruton's
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81	12.8	64.0	37	2	AAAT30023 Primer utl
82	12.8	64.0	42	14	ADJ34425 Human CTL
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ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Homiidae; Homo.

REFERENCE
AUTHORS    Norman,M., Wang,H.L., Rzasa,R., Zhong,W., Nguyen,T. and Kaller,M.
TITLE      Quinolone derivatives for treating cell proliferation related
            disorders
JOURNAL    Patent: WO 0306630-A 1 14-AUG-2003;
            Amgen Inc. (US)

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DEFINITION      Sequence 1 from Patent WO03101985.
ACCESSION       AX960556
VERSION         AX960556.1 GI:40880613
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SOURCE          Homo sapiens (human)
ORGANISM        Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Homiidae; Homo.

REFERENCE
AUTHORS        Huang,Q., Kaller,M., Nguyen,T., Norman,M.H., Rzasa,R., Wang,H.L.
            and Zhong,W.
TITLE          2-oxo-1,3,4-trihydroquinazolinyl derivatives for the treatment
            of cell proliferation-related disorders
JOURNAL        Patent: WO 03101985-A 1 11-DEC-2003;
            Amgen Inc. (US)

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DEFINITION AX521235
VERSION AX521235.1 GI:23572083
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1
AUTHORS Nakamura, Y., Sekine, A., Iida, A. and Satto, S.
TITLE Detection of genetic polymorphisms
JOURNAL Patent: WO 02052044-A 7433 04-JUL-2002;
Riken (JP)

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Db

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ACCESSION AX483491
VERSION AX483491.1 GI:22317911
KEYWORDS
SOURCE Candida albicans
ORGANISM Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; mitosporic Saccharomycetales; Candida.

REFERENCE 1
AUTHORS Roemer, T., Jiang, B., Boone, C., Bussey, H. and Olsen, K.L.
TITLE Gene disruption methodologies for drug target discovery
JOURNAL Patent: WO 02053728-A 791 11-JUL-2002;
Eli Lilly Pharmaceuticals, Inc. (US)

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Db 7 TCCCCATTTTATGAAT 24

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ACCESSION CQ769912
VERSION CQ769912.1 GI:45114370
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1
AUTHORS Santora, V., Askew, B.C., de Morin, F.F., Hague, A., Laber, E., Li, A., Liu, G., Lopez, P., Nomak, R., Tegley, C. and Yang, K.
TITLE Thiazolyl urea compounds for the treatment of cancer
JOURNAL Patent: WO 2003070727-A 1 28-AUG-2003;
Amgen Inc. (US)

FEATURES
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Best Local Similarity 83.3%; Pred. No. 2.1e+05;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TCCCCATTTATGAAT 18
28 TCCTCATATTATGAATT 11

Db

RESULT 28
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LOCUS AR194076/c
DEFINITION Sequence 5 from patent US 6348333.
ACCESSION AR194076
VERSION AR194076.1 GI:20240668
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 45)
AUTHORS Niwa, M., Okamoto, M., Matsumoto, T. and Segawa, T.
TITLE VEGF-binding KDR polypeptide
JOURNAL Patent: US 6348333-A 5 19-FEB-2002;
Location/Qualifiers

FEATURES
source location/Qualifiers
1..45
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 66.0%; Score 13.2; DB 6; Length 45;
Best Local Similarity 83.3%; Pred. No. 2.1e+05;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TCCCCATTTATGAAT 18
25 TCCTCATATTATAGAT 8

Db

RESULT 29
AX816400/c 45 bp DNA linear PAT 09-DEC-2003
LOCUS AX816400
DEFINITION Sequence 1 from Patent WO03066630.
ACCESSION AX816400
VERSION AX816400.1 GI:39646875

RESULT 20
AX197320/c
LOCUS AX197320 26 bp DNA linear PAT 07-SEP-2001
DEFINITION Sequence 1027 from Patent WO0151627.
ACCESSION AX197320
VERSION AX197320.1 GI:15387526
KEYWORDS
SOURCE Glycine max (soybean)
ORGANISM Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.
REFERENCE
AUTHORS Hauge,B.M., Wang,M.L., Parsons,J.D. and Parnell,L.D.
TITLE Nucleic acid molecules and other molecules associated with soybean
JOURNAL cyst nematode resistance
PATENT: WO 0151627-A 1027 19-JUL-2001;
MONSANTO COMPANY (US)
FEATURES
source Location/Qualifiers
1..26
/organism="Glycine max"
/mol_type="unassigned DNA"
/db_xref="taxon:3847"
/note="Seq ID: 515002_region_G2_5089_14_Forward_Primer"
ORIGIN
Query Match 66.0%; Score 13.2; DB 6; Length 26;
Best Local Similarity 83.3%; Pred. No. 2.3e+05;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 3 CCCCATTATTATGGAATGA 20
Db 18 CCGATATTTTCAGGTATGA 1
RESULT 21
AX792594 30 bp DNA linear PAT 17-JUL-2003
LOCUS AX792594
DEFINITION Sequence 5058 from Patent WO02066501.
ACCESSION AX792594
VERSION AX792594.1 GI:32958041
KEYWORDS
SOURCE Helicobacter pylori
ORGANISM Helicobacter pylori
Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
Helicobacteraceae; Helicobacter.
REFERENCE
AUTHORS Legrain,P., Rain,J.C., Colland,F., de Reuse,H. and Labigne,A.
TITLE Protein-protein interactions in Helicobacter pylori
JOURNAL Patent: WO 02066501-A 5058 29-AUG-2002;
Hybrigenics (FR); INSTITUT PASTEUR (FR)
FEATURES
source Location/Qualifiers
1..30
/organism="Helicobacter pylori"
/mol_type="unassigned DNA"
/db_xref="taxon:210"
ORIGIN
Query Match 66.0%; Score 13.2; DB 6; Length 30;
Best Local Similarity 83.3%; Pred. No. 2.2e+05;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2 CCCCATTATTATGGAATG 19
Db 13 CCGCTATTATTATGATG 30
RESULT 22
CQ903062 35 bp DNA linear PAT 16-NOV-2004
LOCUS CQ903062
DEFINITION Sequence 9 from Patent WO2004093919.
ACCESSION CQ903062

VERSION CQ903062.1 GI:55784904
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE
AUTHORS Laman,H.
TITLE Target for cancer therapy and drug discovery
JOURNAL Patent: WO 2004093919-A 9 04-NOV-2004;
University College London (GB)
FEATURES
source Location/Qualifiers
1..35
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="PCR primer"
ORIGIN
Query Match 66.0%; Score 13.2; DB 6; Length 35;
Best Local Similarity 83.3%; Pred. No. 2.2e+05;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 TCCCCATTATTATGGAAT 18
Db 15 TGCCCATATTATTGGAAT 32
RESULT 23
AR119628/c 38 bp DNA linear PAT 16-MAY-2001
LOCUS AR119628
DEFINITION Sequence 17 from patent US 6153397.
ACCESSION AR119628
VERSION AR119628.1 GI:14102327
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
AUTHORS Wisniewski,N., Silver,G.M., Lo,K.Callies. and Brandt,K.S.
TITLE Flea epoxide hydrolase proteins and uses thereof
JOURNAL Patent: US 6153397-A 17 28-NOV-2000;
FEATURES
source Location/Qualifiers
1..38
/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN
Query Match 66.0%; Score 13.2; DB 6; Length 38;
Best Local Similarity 83.3%; Pred. No. 2.1e+05;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 TCCCCATTATTATGGAAT 18
Db 23 TACCCATATTATTAGGAT 6
RESULT 24
AR169109/c 38 bp DNA linear PAT 17-DEC-2001
LOCUS AR169109
DEFINITION Sequence 17 from patent US 6290958.
ACCESSION AR169109
VERSION AR169109.1 GI:17906863
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE
AUTHORS Wisniewski,N., Silver,G.M., Lo,K.Callies. and Brandt,K.S.
TITLE Anti-flea epoxide hydrolase antibodies and uses thereof
JOURNAL Patent: US 6290958-A 17 18-SEP-2001;
FEATURES
source Location/Qualifiers
1..38
/organism="unknown"

REFERENCE 1 (bases 1 to 21)
AUTHORS Sukhame,V.P.
TITLE Methods and materials relating to the functional domains of DNA binding proteins
JOURNAL Patent: US 5763209-A 45 09-JUN-1998;
FEATURES location/Qualifiers
source 1..21
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 66.0%; Score 13.2; DB 6; Length 21;
Best Local Similarity 83.3%; Pred. No. 2.4e+05;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 TCCCCATATTATGGAAT 18
19 TCCCCATATTATGGAAT 2

Db 19 TCCCCATATTATGGAAT 2

RESULT 16
AR014537 21 bp DNA linear PAT 05-DEC-1998
LOCUS Sequence 45 from patent US 5773583.
DEFINITION AR014537
ACCESSION AR014537
VERSION AR014537.1 GI:3971991
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 21)
AUTHORS Sukhame,V.P.
TITLE Methods and materials relating to the functional domains of DNA binding proteins
JOURNAL Patent: US 5773583-A 45 30-JUN-1998;
FEATURES location/Qualifiers
source 1..21
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 66.0%; Score 13.2; DB 6; Length 21;
Best Local Similarity 83.3%; Pred. No. 2.4e+05;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 TCCCCATATTATGGAAT 18
19 TCCCCATATTATGGAAT 2

Db 19 TCCCCATATTATGGAAT 2

RESULT 17
CS013326 21 bp DNA linear PAT 11-FEB-2005
LOCUS Sequence 3251 from Patent WO2005007144.
DEFINITION CS013326
ACCESSION CS013326
VERSION CS013326.1 GI:59673141
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1
Hakonarson,H., Gurney,M.E. and Halapi,E.
AUTHORS Methods of diagnosis and treatment for asthma based on haplotype association
TITLE Patent: WO 2005007144-A 3251 27-JAN-2005;
JOURNAL Decode Genetics EHF. (15)
FEATURES location/Qualifiers
source 1..21
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

Query Match 66.0%; Score 13.2; DB 6; Length 21;
Best Local Similarity 83.3%; Pred. No. 2.4e+05;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 CCCCATATTATGGAAT 19
3 CCCCATATTATGGAAT 20

Db 3 CCCCATATTATGGAAT 20

RESULT 18
A23924 26 bp DNA linear PAT 25-JAN-1995
LOCUS TGF-beta hybrid PCR primer.
DEFINITION A23924
ACCESSION A23924
VERSION A23924.1 GI:833318
KEYWORDS
SOURCE Synthetic construct
ORGANISM Synthetic construct
other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 26)
AUTHORS McMaster,G.K., Cox,D., Cerletti,N. and Kuhla,J.
TITLE Novel hybrid transforming growth factors
JOURNAL Patent: EP 0542679-A 30 19-MAY-1993;
FEATURES CIBA-GEIGY AG
source 1..26
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

ORIGIN

Query Match 66.0%; Score 13.2; DB 6; Length 26;
Best Local Similarity 83.3%; Pred. No. 2.3e+05;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 TCCCCATATTATGGAAT 18
1 TCCCCATATTATGGAAT 18

Db 1 TCCCCATATTATGGAAT 18

RESULT 19
A23925 26 bp DNA linear PAT 25-JAN-1995
LOCUS TGF-beta hybrid PCR primer.
DEFINITION A23925
ACCESSION A23925
VERSION A23925.1 GI:833319
KEYWORDS
SOURCE Synthetic construct
ORGANISM Synthetic construct
other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 26)
AUTHORS McMaster,G.K., Cox,D., Cerletti,N. and Kuhla,J.
TITLE Novel hybrid transforming growth factors
JOURNAL Patent: EP 0542679-A 31 19-MAY-1993;
FEATURES CIBA-GEIGY AG
source 1..26
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

ORIGIN

Query Match 66.0%; Score 13.2; DB 6; Length 26;
Best Local Similarity 83.3%; Pred. No. 2.3e+05;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 TCCCCATATTATGGAAT 18
26 TCCCCATATTATGGAAT 9

Db 26 TCCCCATATTATGGAAT 9

TITLE Direct Submission
JOURNAL Submitted (21-NOV-2002) Balzergue S., UMRGV, INRA/CNRS, 2 rue Gaston Cremieux, 91057 Evry cedex, FRANCE
COMMENT PCR was performed on DNA from transformants of Arabidopsis thaliana plants from INRA (Versailles). The DNA fragment(s) resulting from the PCR were directly sequenced from the left or the right border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at <http://dbsgap.versailles.inra.fr/publiclines/>. This sequence has been generated in the framework of the French plant genomics program "Genoplante" (<http://www.genoplante.com> and <http://genoplante-info.inbio.gen.fr>).

FEATURES
source
1..42
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/db_xref="taxon:3702"
/clone_1id="336E02"
/ecotype="Massillewskija"
/note="T-DNA flanking sequence
left border"

misc_feature
1..42
/note="T-DNA flanking sequence
left border"

ORIGIN

Query Match 67.0%; Score 13.4; DB 15; Length 42;
Best Local Similarity 93.3%; Pred. No. 1.7e+05;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 ATATTATGGAATGA 20
|||||
7 ATATTATGGAATGA 21

Db 7 ATATTATGGAATGA 21

RESULT 12
LOCUS AR284803 47 bp DNA linear PAT 10-APR-2003
DEFINITION Sequence 855 from patent US 6528260.
ACCESSION AR284803
VERSION AR284803.1 GI:29721707
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 47)
AUTHORS Blumentfeld,M., Chumakov,I., Bougueleret,I. and Cohen,A.
TITLE Biallelic markers related to genes involved in drug metabolism
JOURNAL Patent: US 6528260-A 855 04-MAR-2003;
Genet, S.A.;;
FRX;

FEATURES
source
1..47
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Query Match 67.0%; Score 13.4; DB 6; Length 47;
Best Local Similarity 82.4%; Pred. No. 1.7e+05;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 TCCCATATTATGGA 17
|:|||||
21 TCCCATATTATGGA 37

Db 21 TCCCATATTATGGA 37

RESULT 13
LOCUS AX162384 51 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 5712 from Patent WO0140521.
ACCESSION AX162384
VERSION AX162384.1 GI:14543715

KEYWORDS Homo sapiens (human)
SOURCE
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae; Homo.

REFERENCE 1
AUTHORS Shimkets,R.A. and Leach,M.
TITLE Nucleic acids containing single nucleotide polymorphisms and methods of use thereof
JOURNAL Patent: WO 0140521-A 5712 07-JUN-2001;
Curagen Corporation (US)
FEATURES
source
1..51
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
26
/note="2 of 2 allelic variants (5711 is other entry)
Accession number CG4403776"

misc_feature
Accession number CG4403776"

ORIGIN

Query Match 67.0%; Score 13.4; DB 6; Length 51;
Best Local Similarity 93.3%; Pred. No. 1.6e+05;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 ATATTATGGAATGA 20
|||||
27 AGATTATGGAATGA 13

Db 27 AGATTATGGAATGA 13

RESULT 14
LOCUS AR370235 20 bp DNA linear PAT 12-SEP-2003
DEFINITION Sequence 56 from patent US 6300132.
ACCESSION AR370235
VERSION AR370235.1 GI:34606741
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Montia,B.P. and Cowser,T.M.
TITLE Antisense inhibition of telomeric repeat binding factor 2 expression
JOURNAL Patent: US 6300132-A 56 09-OCT-2001;
Isis Pharmaceuticals, Inc.; Carlsbad, CA;
WOX;

FEATURES
source
1..20
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Query Match 66.0%; Score 13.2; DB 6; Length 20;
Best Local Similarity 83.3%; Pred. No. 2.4e+05;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TCCCATATTATGGA 18
|||||
3 TCCCATATTATGGA 20

Db 3 TCCCATATTATGGA 20

RESULT 15
LOCUS AR012098 21 bp DNA linear PAT 04-DEC-1998
DEFINITION Sequence 45 from patent US 5763209.
ACCESSION AR012098
VERSION AR012098.1 GI:3970088
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

DEFINITION Brucella abortus clone pUD51 putative promoter region.
ACCESSION AF072570
VERSION AF072570.1 GI:3309189
KEYWORDS
SOURCE
ORGANISM Brucella melitensis biovar Abortus (Brucella abortus)
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Brucellaceae; Brucella.
REFERENCE
AUTHORS 1 (bases 1 to 74)
TITLE Dai, J., and Essenberg, R.C.
DNA drives expression of luciferase in Brucella abortus 2308 on tryptose and erythritol but not glucose, galactose, or succinate
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 74)
AUTHORS Dai, J., and Essenberg, R.C.
TITLE Direct Submission
JOURNAL Submitted (19-JUN-1998) Department of Biochemistry and Molecular Biology, Oklahoma State University, Stillwater, OK 74078-3035, USA
FEATURES
source
1. .74
/organism="Brucella melitensis biovar Abortus"
/mol_type="genomic DNA"
/strain="2308"
/db_xref="taxon:235"
/clone="pUD51"
1. .74
/note="putative; drives expression of reporter gene on tryptose and erythritol but not glucose, galactose, or succinate"
ORIGIN
promoter
Query Match 68.0%; Score 13.6; DB 1; Length 74;
Best Local Similarity 80.0%; Pred. No. 1.2e+05;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 1 TCCCCATTTTATGGAATGA 20
Db 52 TTCCGATATATATGGAAGA 33
RESULT 9
LOCUS AY728578 75 bp DNA linear PRI 02-MAR-2005
DEFINITION Macaca mulatta isolate SIV_RQ3556_6p21.32c SIV-derived vector proviral integration site.
ACCESSION AY728578
VERSION AY728578.1 GI:51947696
KEYWORDS
SOURCE Macaca mulatta (rhesus monkey)
ORGANISM Macaca mulatta
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Cercopithecoidea; Cercopithecoidea; Macaca.
REFERENCE
AUTHORS 1 (bases 1 to 75)
TITLE Hematti, P., Hong, B.-K., Ferguson, C., Adler, R., Hanawa, H., Sellers, S., Holt, I.E., Eckfeldt, C.E., Sharma, Y., Schmidt, M., von Kalle, C., Persons, D.A., Billings, E.M., Verfalli, C.M., Nienhuis, A.W., Wolfberg, T.G., Dunbar, C.E. and Calmels, B.
Distinct genomic integration of MLV and SIV vectors in primate hematopoietic stem and progenitor cells
JOURNAL PLOS Biol. 2 (12), E423 (2004)
PUBMED 15550989
REFERENCE 2 (bases 1 to 75)
AUTHORS Hematti, P., Hong, B.-K., Ferguson, C., Adler, R., Sellers, S., Dunbar, C.E. and Calmels, B.
TITLE Direct Submission
JOURNAL Submitted (19-AUG-2004) Hematology Branch, NHLBI/NIH, 10 Center Drive, Bethesda, MD 20892, USA
FEATURES
source
1. .75
/organism="Macaca mulatta"
/mol_type="genomic DNA"
/isolate="SIV_RQ3556_6p21.32c"

/db_xref="taxon:9544"
/cell_type="circulating granulocytes and mononuclear cells"
misc_feature
1. .75
/note="SIV-derived vector proviral integration site"
ORIGIN
Query Match 68.0%; Score 13.6; DB 8; Length 75;
Best Local Similarity 80.0%; Pred. No. 1.2e+05;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 1 TCCCCATTTTATGGAATGA 20
Db 10 TACTATATTTTGTGGAATGA 29
RESULT 10
LOCUS CS010423/c 26 bp DNA linear PAT 11-FEB-2005
DEFINITION Sequence 348 from Patent WO2005007144.
ACCESSION CS010423
VERSION CS010423.1 GI:59670238
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.
REFERENCE
AUTHORS 1
TITLE Hakonarson, H., Gurney, M.E. and Halapi, B.
Methods of diagnosis and treatment for asthma based on haplotype association
JOURNAL Patent: WO 2005007144-A 348 27-JAN-2005;
FEATURES
source
1. .26
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN
Query Match 67.0%; Score 13.4; DB 6; Length 26;
Best Local Similarity 93.3%; Pred. No. 1.8e+05;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 6 ATATTATGGAATGA 20
Db 17 ATATTATGGAATGA 3
RESULT 11
LOCUS ATH552444 42 bp DNA linear PLN 29-MAR-2003
DEFINITION Arabidopsis thaliana T-DNA flanking sequence, left border, clone 336E02.
ACCESSION ATH552444
VERSION ATH552444.1 GI:29368589
KEYWORDS left border; T-DNA flanking sequence.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE
AUTHORS 1
TITLE Brunaud, V., Balzerque, S., Dubreucq, B., Aubourg, S., Samson, F., Chauvin, S., Bechtold, N., Cruaud, C., DePOSE, R., Pelletier, G., Lepoint, L., Caboche, M. and Lecharny, A.
T-DNA integration into the Arabidopsis genome depends on sequences of pre-insertion sites
JOURNAL EMBO Rep. 3 (12), 1152-1157 (2002)
PUBMED 12446565
REFERENCE 2 (bases 1 to 42)
AUTHORS Balzerque, S.

Query Match 71.0%; Score 14.2; DB 10; Length 77;
Best Local Similarity 84.2%; Pred. No. 6.4e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 TCCCATATTATGGAATGA 19
Db 32 TCCACATATTATGGAACG 50

RESULT 4
LOCUS AX791547 30 bp DNA linear PAT 17-JUL-2003
DEFINITION Sequence 4011 from Patent WO02066501.
ACCESSION AX791547
VERSION AX791547.1 GI:32956994
KEYWORDS
SOURCE Helicobacter pylori
ORGANISM Helicobacter pylori
Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
Helicobacteraceae; Helicobacter.

REFERENCE 1
Legrain, P., Rain, J.C., Colland, F., de Reuse, H. and Labigne, A.
Protein-protein interactions in Helicobacter pylori
Patent: WO 02066501-A 4011 29-AUG-2002;
Hydrigenics (FR); INSTITUT PASTEUR (FR)

FEATURES
source location/Qualifiers
1..30
/organism="Helicobacter pylori"
/mol_type="unassigned DNA"
/db_xref="taxon:210"

ORIGIN

Query Match 68.0%; Score 13.6; DB 6; Length 30;
Best Local Similarity 80.0%; Pred. No. 1.4e+05;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 TCCCATATTATGGAATGA 20
Db 25 TCACATTATTCATGGAATGA 6

RESULT 5
LOCUS CQ814459 40 bp DNA linear PAT 24-MAY-2004
DEFINITION Sequence 820 from Patent WO2004035819.
ACCESSION CQ814459
VERSION CQ814459.1 GI:47603663
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.

REFERENCE 1
Kauppinen, S., Alsbö, C., Nielsen, P.S., Jeffares, D.C., Mourier, T.,
Arcander, P., Tommerup, N., Tølerup, N. and Vissing, H.
Oligonucleotides useful for detecting and analyzing nucleic acid of
interest
Patent: WO 2004035819-A 820 29-APR-2004;
Exigon A/S (DK)

FEATURES
source location/Qualifiers
1..40
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic oligonucleotide sequence"

ORIGIN

Query Match 68.0%; Score 13.6; DB 6; Length 40;
Best Local Similarity 80.0%; Pred. No. 1.4e+05;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 TCCCATATTATGGAATGA 20
Db 34 TTCACATATTATTCATGGA 15

RESULT 6
LOCUS CQ814451/c 50 bp DNA linear PAT 24-MAY-2004
DEFINITION Sequence 812 from Patent WO2004035819.
ACCESSION CQ814451
VERSION CQ814451.1 GI:47603655
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.

REFERENCE 1
Kauppinen, S., Alsbö, C., Nielsen, P.S., Jeffares, D.C., Mourier, T.,
Arcander, P., Tommerup, N., Tølerup, N. and Vissing, H.
Oligonucleotides useful for detecting and analyzing nucleic acid of
interest
Patent: WO 2004035819-A 812 29-APR-2004;
Exigon A/S (DK)

FEATURES
source location/Qualifiers
1..50
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic oligonucleotide sequence"

ORIGIN

Query Match 68.0%; Score 13.6; DB 6; Length 50;
Best Local Similarity 80.0%; Pred. No. 1.3e+05;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 TCCCATATTATGGAATGA 20
Db 39 TTCACATATTATTCATGGA 20

RESULT 7
LOCUS CQ557319 65 bp DNA linear PAT 30-JAN-2004
DEFINITION Sequence 26954 from Patent WO0210449.
ACCESSION CQ557319
VERSION CQ557319.1 GI:41523746
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE 1
Shoshan, A., Maesman, A., Mintz, E., Mintz, L. and Paigler, S.
Oligonucleotide library for detecting rna transcripts and splice
variants that populate a transcriptome
Patent: WO 0210449-A 26954 07-FEB-2002;
Comugen Inc. (US)

FEATURES
source location/Qualifiers
1..65
/organism="Mus musculus"
/mol_type="unassigned DNA"
/db_xref="taxon:10090"

ORIGIN

Query Match 68.0%; Score 13.6; DB 6; Length 65;
Best Local Similarity 80.0%; Pred. No. 1.3e+05;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 TCCCATATTATGGAATGA 20
Db 12 TCCTCATATTCTTCGAGTCA 31

RESULT 8
LOCUS AF072570/c 74 bp DNA linear BCT 11-JUL-1998
AF072570


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c 92 12.4 62.0 80 6 CQ152403 Sequence
c 93 12.4 62.0 80 6 CQ185747 Sequence
c 94 12.4 62.0 80 6 CQ235737 Sequence
c 95 12.4 62.0 80 6 CQ273310 Sequence
c 96 12.4 62.0 80 6 CQ310741 Sequence
c 97 12.4 62.0 80 6 CQ347599 Sequence
c 98 12.2 61.0 19 6 CS009771 Sequence
c 99 12.2 61.0 19 6 CS009857 Sequence
100 12.2 61.0 20 6 AR241059 AR241059 Sequence

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ALIGNMENTS

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RESULT 1
AXI62383/c
LOCUS AXI62383 51 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 5711 from Patent WO0140521.
ACCESSION AXI62383
VERSION AXI62383.1 GI:14543714
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominae; Homo.

```

```

REFERENCE
AUTHORS Shinkets, R.A. and Leach, M.
TITLE Nucleic acids containing single nucleotide polymorphisms and
methods of use thereof
JOURNAL Patent: WO 0140521-A 5711 07-JUN-2001;
Curagen Corporation (US)
FEATURES
source 1..51
Location/Qualifiers
1..51
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
26
/note="1 of 2 allelic variants (5712 is other entry)
Accession number CG44023776"

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ORIGIN
misc_feature
Accession number CG44023776"
Query Match 75.0%; Score 15; DB 6; Length 51;
Best Local Similarity 100.0%; Pred. No. 2.8e+04;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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CY 6 ATATTATGGAATGA 20
Db 27 ATATTATGGAATGA 13

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RESULT 2
AL807567 68 bp DNA linear STS 10-JUN-2003
LOCUS AL807567 Arabidopsis thaliana transposon insertion STS SM_3.20845, sequence
tagged site.
ACCESSION AL807567
VERSION AL807567.1 GI:21628283
KEYWORDS STS; STS, sequence tagged site.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis..
REFERENCE
AUTHORS Clarke, J.H., Bowles, B., Carter, J., Hart, D., McCullagh, B.,
Murphy, G., Langham, S., Legrys, C., Jones, J.D.G. and Bevan, M.
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 68)
AUTHORS Clarke, J.H.
TITLE Direct Submision
JOURNAL Submitted (27-JUN-2002) Clarke J.H., John Innes Centre, Colney
Lane, Norwich, NR4 7UJ, UK

```

COMMENT

AT denotes an activation tag dissociation transposon within a single line. ET an enhancer trap dissociation transposon. GT a gene trap dissociation transposon. MT a mis-expression enhancer trap dissociation transposon. SM a defective suppressor mutator transposon. _3 denotes a sequence derived from the 3' end of the transposon. _5 denotes a sequence derived from the 5' end of the transposon. BSRG GARNET, ARIS project

FEATURES

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source
Location/Qualifiers
1..68
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/variety="Columbia-0 NASC stock code N1092"
/db_xref="taxon:3702"
/clone="AC002328"
/note="Derived from superpool 16.38 NASC code N40733"
1..68
/standard_name="SM_3.20845"

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ORIGIN

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Query Match 71.0%; Score 14.2; DB 10; Length 68;
Best Local Similarity 84.2%; Pred. No. 6.5e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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CY 1 TCCCATTTTATGGAATG 19
Db 32 TCCCAAAATTTATGGAACG 50

```

```

RESULT 3
AL834013 77 bp DNA linear STS 10-JUN-2003
LOCUS AL834013 Arabidopsis thaliana transposon insertion STS SM_3.20924, sequence
tagged site.
ACCESSION AL834013
VERSION AL834013.1 GI:21738849
KEYWORDS STS; STS, sequence tagged site.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

```

```

REFERENCE
AUTHORS Clarke, J.H., Bowles, B., Carter, J., Hart, D., McCullagh, B.,
Murphy, G., Langham, S., Legrys, C., Jones, J.D.G. and Bevan, M.
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 77)
AUTHORS Clarke, J.H.
TITLE Direct Submision
JOURNAL Submitted (11-JUL-2002) Clarke J.H., John Innes Centre, Colney
Lane, Norwich, NR4 7UJ, UK

```

COMMENT

AT denotes an activation tag dissociation transposon within a single line. ET an enhancer trap dissociation transposon. GT a gene trap dissociation transposon. MT a mis-expression enhancer trap dissociation transposon. SM a defective suppressor mutator transposon. _3 denotes a sequence derived from the 3' end of the transposon. _5 denotes a sequence derived from the 5' end of the transposon. BSRG GARNET, ARIS project

FEATURES

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source
Location/Qualifiers
1..77
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/variety="Columbia-0 NASC stock code N1092"
/db_xref="taxon:3702"
/clone="AC002328"
/note="Derived from superpool 16.44 NASC code N40739"
1..77
/standard_name="SM_3.20924"

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ORIGIN

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 1, 2006, 22:25:24 ; Search time 589.333 Seconds
(without alignments)
1929.076 Million cell updates/sec

Title: us-10-653-528-37

Perfect score: 20

Sequence: 1 tccccattatcgaatga 20

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 2389942

Minimum DB seq length: 0
Maximum DB seq length: 80

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database :

GenBml:*
1: gb_da:*
2: gb_in:*
3: gb_env:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pr:*
9: gb_ro:*
10: gb_sts:*
11: gb_sy:*
12: gb_un:*
13: gb_vl:*
14: gb_htg:*
15: gb_pl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	* Query Match	Length	DB	ID	Description
1	15	75.0	51	6	AX162383	AX162383 Sequence
2	14.2	71.0	68	10	AL807567	AL807567 Arabidops
3	14.2	71.0	77	10	AL834013	AL834013 Arabidops
4	13.6	68.0	30	6	AX791547	AX791547 Sequence
5	13.6	68.0	40	6	CQ814451	CQ814451 Sequence
6	13.6	68.0	50	6	CQ814451	CQ814451 Sequence
7	13.6	68.0	65	6	CQ557319	CQ557319 Sequence
8	13.6	68.0	74	1	AF072570	AF072570 Brucella
9	13.6	68.0	75	8	AY728578	AY728578 Macaca mu
10	13.4	67.0	26	6	CS010423	CS010423 Sequence
11	13.4	67.0	42	15	ATHS5244	ATHS5244 Arabidops
12	13.4	67.0	47	6	AR284803	AR284803 Sequence
13	13.4	67.0	51	6	AX162384	AX162384 Sequence
14	13.2	66.0	20	6	AR370235	AR370235 Sequence
15	13.2	66.0	21	6	AR012098	AR012098 Sequence
16	13.2	66.0	21	6	AR014537	AR014537 Sequence
17	13.2	66.0	21	6	CS013326	CS013326 Sequence
18	13.2	66.0	26	6	A23924	TGF-beta hy

C 19	13.2	66.0	26	6	A23925	A23925 TGF-beta hy
C 20	13.2	66.0	26	6	AX197320	AX197320 Sequence
C 21	13.2	66.0	30	6	AX792594	AX792594 Sequence
C 22	13.2	66.0	35	6	CQ903062	CQ903062 Sequence
C 23	13.2	66.0	38	6	AR119628	AR119628 Sequence
C 24	13.2	66.0	38	6	AR169109	AR169109 Sequence
C 25	13.2	66.0	41	6	AX521235	AX521235 Sequence
C 26	13.2	66.0	41	6	AX483491	AX483491 Sequence
C 27	13.2	66.0	45	6	CQ769912	CQ769912 Sequence
C 28	13.2	66.0	45	6	AR194076	AR194076 Sequence
C 29	13.2	66.0	45	6	AX816400	AX816400 Sequence
C 30	13.2	66.0	47	6	AX960556	AX960556 Sequence
C 31	13.2	66.0	47	6	AR288988	AR288988 Sequence
C 32	13.2	66.0	60	6	CQ547660	CQ547660 Sequence
C 33	13	65.0	24	6	AR307538	AR307538 Sequence
C 34	13	65.0	42	6	AR648197	AR648197 Sequence
C 35	12.8	64.0	21	6	AX153847	AX153847 Sequence
C 36	12.8	64.0	31	6	AR076838	AR076838 Sequence
C 37	12.8	64.0	31	6	AR172659	AR172659 Sequence
C 38	12.8	64.0	31	6	AR218146	AR218146 Sequence
C 39	12.8	64.0	31	6	AR592405	AR592405 Sequence
C 40	12.8	64.0	31	6	AR634647	AR634647 Sequence
C 41	12.8	64.0	33	6	I30467	I30467 Sequence 12
C 42	12.8	64.0	33	6	AX718907	AX718907 Sequence
C 43	12.8	64.0	33	6	AX718908	AX718908 Sequence
C 44	12.8	64.0	37	6	A50800	A50800 Sequence 21
C 45	12.8	64.0	37	6	AR109991	AR109991 Sequence
C 46	12.8	64.0	42	6	CS037312	CS037312 Sequence
C 47	12.8	64.0	47	6	CQ655019	CQ655019 Sequence
C 48	12.8	64.0	50	6	AX162206	AX162206 Sequence
C 49	12.8	64.0	60	6	CQ552375	CQ552375 Sequence
C 50	12.8	64.0	60	6	CQ552803	CQ552803 Sequence
C 51	12.8	64.0	65	6	CQ532680	CQ532680 Sequence
C 52	12.8	64.0	65	6	CQ560639	CQ560639 Sequence
C 53	12.8	64.0	65	6	AX482987	AX482987 Sequence
C 54	12.8	64.0	68	10	BX295087	BX295087 Arabidops
C 55	12.8	64.0	72	9	MUSDHPR1	M10722 Mouse dihyd
C 56	12.8	64.0	73	6	BD226440	BD226440 Immunosup
C 57	12.8	64.0	73	6	AX011090	AX011090 Sequence
C 58	12.8	64.0	76	6	BD226437	BD226437 Immunosup
C 59	12.8	64.0	76	6	AX011087	AX011087 Sequence
C 60	12.6	63.0	20	6	CQ943432	CQ943432 Sequence
C 61	12.6	63.0	20	6	AR313846	AR313846 Sequence
C 62	12.6	63.0	21	6	AR299001	AR299001 Sequence
C 63	12.6	63.0	27	6	CQ787126	CQ787126 Sequence
C 64	12.6	63.0	31	6	AR069154	AR069154 Sequence
C 65	12.6	63.0	31	6	I49575	I49575 Sequence 24
C 66	12.6	63.0	40	6	CQ814479	CQ814479 Sequence
C 67	12.6	63.0	43	6	AX484434	AX484434 Sequence
C 68	12.6	63.0	44	6	AR110223	AR110223 Sequence
C 69	12.6	63.0	44	6	AR169982	AR169982 Sequence
C 70	12.6	63.0	44	6	AR171791	AR171791 Sequence
C 71	12.6	63.0	44	6	BD189485	BD189485 PROMOTER
C 72	12.6	63.0	44	6	AR264128	AR264128 Sequence
C 73	12.6	63.0	44	6	BD009016	BD009016 Promoter
C 74	12.6	63.0	45	6	BD091342	BD091342 In vitro
C 75	12.6	63.0	49	6	AX081672	AX081672 Sequence
C 76	12.6	63.0	51	6	CQ814467	CQ814467 Sequence
C 77	12.6	63.0	51	6	AR064026	AR064026 Sequence
C 78	12.6	63.0	51	6	BD059966	BD059966 Chlorella
C 79	12.6	63.0	51	6	AR372733	AR372733 Sequence
C 80	12.6	63.0	52	6	AR609406	AR609406 Sequence
C 81	12.6	63.0	65	6	CQ556890	CQ556890 Sequence
C 82	12.6	63.0	68	2	AY449504	AY449504 Campanile
C 83	12.6	63.0	78	10	BX295688	BX295688 Arabidops
C 84	12.6	63.0	80	10	BX294236	BX294236 Arabidops
C 85	12.4	62.0	17	6	AX762125	AX762125 Sequence
C 86	12.4	62.0	42	6	AR076441	AR076441 Sequence
C 87	12.4	62.0	42	6	AR106041	AR106041 Sequence
C 88	12.4	62.0	60	6	CQ543493	CQ543493 Sequence
C 89	12.4	62.0	65	6	AX483865	AX483865 Sequence
C 90	12.4	62.0	65	6	AX484991	AX484991 Sequence
C 91	12.4	62.0	80	6	CQ113523	CQ113523 Sequence

LENGTH: 19
TYPE: RNA
ORGANISM: Homo sapiens
US-11-101-244-1066281

Query Match 66.0%; Score 13.2; DB 10; Length 19;
Best Local Similarity 66.7%; Pred. No. 9e+02; 3; Indels 0; Gaps 0;
Matches 12; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 3 ATGGAATGATACCGTCAT 20
Db 1 AAGGAAGAAGACAGUCAU 18

RESULT 28

US-11-101-244-1463744/C
Sequence 1463744, Application US/11101244
Publication No. US20050246794A1
GENERAL INFORMATION:
APPLICANT: Dharmacon, Inc.
APPLICANT: Khvorova, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/101,244
CURRENT FILING DATE: 2005-04-07
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 1463744
LENGTH: 19
TYPE: RNA
ORGANISM: Homo sapiens
US-11-101-244-1463744

Query Match 66.0%; Score 13.2; DB 10; Length 19;
Best Local Similarity 83.3%; Pred. No. 9e+02; 3; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 ATGGAATGATACCGTCAT 20
Db 19 ATGATCATATCCATCAT 2

RESULT 29

US-11-083-784-605119/C
Sequence 605119, Application US/11083784
Publication No. US20050245475A1
GENERAL INFORMATION:
APPLICANT: Dharmacon, Inc.
APPLICANT: Khvorova, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/083,784
CURRENT FILING DATE: 2005-03-18
PRIOR APPLICATION NUMBER: US/10/714,333
PRIOR FILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary

SEQ ID NO 605119
LENGTH: 19
TYPE: RNA
ORGANISM: Homo sapiens
US-11-083-784-605119

Query Match 66.0%; Score 13.2; DB 11; Length 19;
Best Local Similarity 83.3%; Pred. No. 9e+02; 3; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 TTATGGAATGATACCGTC 18
Db 18 TTGTGGAAGACACCGTC 1

RESULT 30

US-11-083-784-1066281
Sequence 1066281, Application US/11083784
Publication No. US20050245475A1
GENERAL INFORMATION:
APPLICANT: Dharmacon, Inc.
APPLICANT: Khvorova, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/083,784
CURRENT FILING DATE: 2005-03-18
PRIOR APPLICATION NUMBER: US/10/714,333
PRIOR FILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 1066281
LENGTH: 19
TYPE: RNA
ORGANISM: Homo sapiens
US-11-083-784-1066281

Query Match 66.0%; Score 13.2; DB 11; Length 19;
Best Local Similarity 66.7%; Pred. No. 9e+02; 3; Indels 0; Gaps 0;
Matches 12; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 3 ATGGAATGATACCGTCAT 20
Db 1 AAGGAAGAAGACAGUCAU 18

Search completed: March 2, 2006, 01:39:35
Job time : 498.333 secs

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; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 293095
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Probe
; US-11-136-527-293095
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Query Match          67.0%; Score 13.4; DB 12; Length 25;
Best Local Similarity 93.3%; Pred. No. 7.4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Qy      1 TTATGATGATACC 15
Db      1 TTATGATGATACC 15
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RESULT 24
; Sequence 293123, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 293123
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Probe
; US-11-136-527-293123
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Query Match          67.0%; Score 13.4; DB 12; Length 25;
Best Local Similarity 93.3%; Pred. No. 7.4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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```
Qy      1 TTATGATGATACC 15
Db      8 TTATGATGATACC 22
```

```

RESULT 25
; Sequence 30250, Application US/11175859
; Publication No. US20060024715A1
; GENERAL INFORMATION:
; APPLICANT: Affymetrix, Inc.
; APPLICANT: Liu, Guoying et al.
; TITLE OF INVENTION: Method of Analysis of Human Polymorphism
; FILE REFERENCE: 3690.1
; CURRENT APPLICATION NUMBER: US/11/175,859
; CURRENT FILING DATE: 2005-07-05
; PRIOR APPLICATION NUMBER: US 60/585,352
; PRIOR FILING DATE: 2004-07-02
; NUMBER OF SEQ ID NOS: 116251
; SOFTWARE: PatentIn version 3.2
```

```

; SEQ ID NO 30250
; LENGTH: 50
; TYPE: DNA
; ORGANISM: homo sapien
; US-11-175-859-30250
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Query Match          67.0%; Score 13.4; DB 12; Length 50;
Best Local Similarity 82.4%; Pred. No. 8.6e+02;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
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```
Qy      4 TGGATGATACCGCTCAT 20
Db      38 TGGATGATACCGCTCTT 22
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```

RESULT 26
; Sequence 605119, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmcon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 605119
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
; US-11-101-244-605119
```

```

Query Match          66.0%; Score 13.2; DB 10; Length 19;
Best Local Similarity 83.3%; Pred. No. 9e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
Qy      1 TTATGATGATACCGCTC 18
Db      18 TTGTGGAGGACACCGCTC 1
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```

RESULT 27
; Sequence 1066281, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmcon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1066281
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; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 649079
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-649079

Query Match      67.0%; Score 13.4; DB 12; Length 25;
Best Local Similarity 93.3%; Pred. No. 7.4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTATGGATGATACC 15
    ||||| |||||
Db 7 TTATGGATGATACC 21

RESULT 19
US-11-121-849-649841
; Sequence 649841, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 649841
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-649841

Query Match      67.0%; Score 13.4; DB 12; Length 25;
Best Local Similarity 93.3%; Pred. No. 7.4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTATGGATGATACC 15
    ||||| |||||
Db 9 TTATGGATGATACC 23

RESULT 20
US-11-121-849-649842
; Sequence 649842, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 649842
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-649842

Query Match      67.0%; Score 13.4; DB 12; Length 25;
Best Local Similarity 93.3%; Pred. No. 7.4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTATGGATGATACC 15
    ||||| |||||
```

```
Db 7 TTATGGATGATACC 21

RESULT 21
US-11-136-527-26188/c
; Sequence 26188, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 26188
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Probe
US-11-136-527-26188

Query Match      67.0%; Score 13.4; DB 12; Length 25;
Best Local Similarity 93.3%; Pred. No. 7.4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 ATGGAATGATACCGT 17
    ||||| |||||
Db 19 AAGGAATGATACCGT 5

RESULT 22
US-11-136-527-26191/c
; Sequence 26191, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 26191
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Probe
US-11-136-527-26191

Query Match      67.0%; Score 13.4; DB 12; Length 25;
Best Local Similarity 93.3%; Pred. No. 7.4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 ATGGAATGATACCGT 17
    ||||| |||||
Db 20 AAGGAATGATACCGT 6

RESULT 23
US-11-136-527-293095
; Sequence 293095, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
```

```
/ Sequence 1019090, Application US/11101244
/ Publication No. US20050246794A1
/ GENERAL INFORMATION:
/ APPLICANT: Dharmacon, Inc.
/ APPLICANT: Khvorova, Anastasia
/ APPLICANT: Reynolds, Angela
/ APPLICANT: Leake, Devin
/ APPLICANT: Marshall, William
/ TITLE OF INVENTION: Scaringe, Stephen
/ FILE REFERENCE: 13499US
/ CURRENT APPLICATION NUMBER: US/11/101,244
/ CURRENT FILING DATE: 2005-04-07
/ PRIOR APPLICATION NUMBER: 60/502,050
/ PRIOR FILING DATE: 2003-09-10
/ PRIOR APPLICATION NUMBER: 60/426,137
/ PRIOR FILING DATE: 2002-11-14
/ NUMBER OF SEQ ID NOS: 1591911
/ SOFTWARE: Proprietary
/ SEQ ID NO 1019090
/ LENGTH: 19
/ TYPE: RNA
/ ORGANISM: Homo sapiens
US-11-101-244-1019090
```

```
Query Match 67.0%; Score 13.4; DB 10; Length 19;
Best Local Similarity 66.7%; Pred. No. 6.9e+02;
Matches 10; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy 6 GAATGATACCGTCAT 20
Db 4 GAUGAUACCGUGAU 18
```

```
RESULT 15
US-11-083-784-1019090
/ Sequence 1019090, Application US/11083784
/ Publication No. US20050245475A1
/ GENERAL INFORMATION:
/ APPLICANT: Dharmacon, Inc.
/ APPLICANT: Khvorova, Anastasia
/ APPLICANT: Reynolds, Angela
/ APPLICANT: Leake, Devin
/ APPLICANT: Marshall, William
/ APPLICANT: Scaringe, Stephen
/ TITLE OF INVENTION: Functional and Hyperfunctional siRNA
/ FILE REFERENCE: 13499US
/ CURRENT APPLICATION NUMBER: US/11/083,784
/ CURRENT FILING DATE: 2005-03-18
/ PRIOR APPLICATION NUMBER: US/10/714,333
/ PRIOR FILING DATE: 2003-11-14
/ PRIOR APPLICATION NUMBER: 60/502,050
/ PRIOR FILING DATE: 2003-09-10
/ PRIOR APPLICATION NUMBER: 60/426,137
/ PRIOR FILING DATE: 2002-11-14
/ NUMBER OF SEQ ID NOS: 1591911
/ SOFTWARE: Proprietary
/ SEQ ID NO 1019090
/ LENGTH: 19
/ TYPE: RNA
/ ORGANISM: Homo sapiens
US-11-083-784-1019090
```

```
Query Match 67.0%; Score 13.4; DB 11; Length 19;
Best Local Similarity 66.7%; Pred. No. 6.9e+02;
Matches 10; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy 6 GAATGATACCGTCAT 20
Db 4 GAUGAUACCGUGAU 18
```

RESULT 16

```
US-11-121-849-649077
/ Sequence 649077, Application US/11121849
/ Publication No. US20050272080A1
/ GENERAL INFORMATION:
/ APPLICANT: John Palma
/ TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded
/ FILE REFERENCE: 3684.1
/ CURRENT APPLICATION NUMBER: US/11/121,849
/ CURRENT FILING DATE: 2005-05-03
/ PRIOR APPLICATION NUMBER: 60/567,949
/ PRIOR FILING DATE: 2004-05-03
/ NUMBER OF SEQ ID NOS: 673904
/ SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
/ SEQ ID NO 649077
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Homo sapien
US-11-121-849-649077
```

```
Query Match 67.0%; Score 13.4; DB 12; Length 25;
Best Local Similarity 93.3%; Pred. No. 7.4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy 1 TTATGGATGATACC 15
Db 11 TTATGGATGATACC 25
```

```
RESULT 17
US-11-121-849-649078
/ Sequence 649078, Application US/11121849
/ Publication No. US20050272080A1
/ GENERAL INFORMATION:
/ APPLICANT: John Palma
/ TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded
/ FILE REFERENCE: 3684.1
/ CURRENT APPLICATION NUMBER: US/11/121,849
/ CURRENT FILING DATE: 2005-05-03
/ PRIOR APPLICATION NUMBER: 60/567,949
/ PRIOR FILING DATE: 2004-05-03
/ NUMBER OF SEQ ID NOS: 673904
/ SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
/ SEQ ID NO 649078
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Homo sapien
US-11-121-849-649078
```

```
Query Match 67.0%; Score 13.4; DB 12; Length 25;
Best Local Similarity 93.3%; Pred. No. 7.4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy 1 TTATGGATGATACC 15
Db 9 TTATGGATGATACC 23
```

```
RESULT 18
US-11-121-849-649079
/ Sequence 649079, Application US/11121849
/ Publication No. US20050272080A1
/ GENERAL INFORMATION:
/ APPLICANT: John Palma
/ TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded
/ FILE REFERENCE: 3684.1
/ CURRENT APPLICATION NUMBER: US/11/121,849
/ CURRENT FILING DATE: 2005-05-03
/ PRIOR APPLICATION NUMBER: 60/567,949
/ PRIOR FILING DATE: 2004-05-03
/ NUMBER OF SEQ ID NOS: 673904
```

```
; APPLICANT: Liu, Guoying et al.
; TITLE OF INVENTION: Method of Analysis of Human Polymorphism
; FILE REFERENCE: 3690.1
; CURRENT APPLICATION NUMBER: US/11/175,859
; CURRENT FILING DATE: 2005-07-05
; PRIOR APPLICATION NUMBER: US 60/585,352
; PRIOR FILING DATE: 2004-07-02
; NUMBER OF SEQ ID NOS: 116251
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 31104
; LENGTH: 50
; TYPE: DNA
; ORGANISM: homo sapien
US-11-175-859-31104
```

```
Query Match      69.0%; Score 13.8; DB 12; Length 50;
Best Local Similarity 78.9%; Pred. No. 5.1e+02;
Matches 15; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
```

```
QY      2 TTATGAATGATACCGTCAT 20
        |||||||
Db      13 TAGCGAATGATACCGAAT 31
```

```
RESULT 10
US-11-175-859-108552/c
; Sequence 108552, Application US/11/175859
; Publication No. US20060024715A1
; GENERAL INFORMATION:
; APPLICANT: Affymetrix, Inc.
; APPLICANT: Liu, Guoying et al.
; TITLE OF INVENTION: Method of Analysis of Human Polymorphism
; FILE REFERENCE: 3690.1
; CURRENT APPLICATION NUMBER: US/11/175,859
; CURRENT FILING DATE: 2005-07-05
; PRIOR APPLICATION NUMBER: US 60/585,352
; PRIOR FILING DATE: 2004-07-02
; NUMBER OF SEQ ID NOS: 116251
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 108552
; LENGTH: 50
; TYPE: DNA
; ORGANISM: homo sapien
US-11-175-859-108552
```

```
Query Match      69.0%; Score 13.8; DB 12; Length 50;
Best Local Similarity 78.9%; Pred. No. 5.1e+02;
Matches 15; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
```

```
QY      1 TTATGAATGATACCGTCAT 19
        |||||||
Db      41 TTATGAATGATACCGTCAT 23
```

```
RESULT 11
US-11-121-849-550185/c
; Sequence 550185, Application US/11/121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 550185
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
```

```
US-11-121-849-550185
```

```
Query Match      68.0%; Score 13.6; DB 12; Length 25;
Best Local Similarity 80.0%; Pred. No. 5.7e+02;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
QY      1 TTATGAATGATACCGTCAT 20
        |||||||
Db      25 TTAGGAAAGATACCAACAT 6
```

```
RESULT 12
US-11-175-859-48186/c
; Sequence 48186, Application US/11/175859
; Publication No. US20060024715A1
; GENERAL INFORMATION:
; APPLICANT: Affymetrix, Inc.
; APPLICANT: Liu, Guoying et al.
; TITLE OF INVENTION: Method of Analysis of Human Polymorphism
; FILE REFERENCE: 3690.1
; CURRENT APPLICATION NUMBER: US/11/175,859
; CURRENT FILING DATE: 2005-07-05
; PRIOR APPLICATION NUMBER: US 60/585,352
; PRIOR FILING DATE: 2004-07-02
; NUMBER OF SEQ ID NOS: 116251
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 48186
; LENGTH: 50
; TYPE: DNA
; ORGANISM: homo sapien
US-11-175-859-48186
```

```
Query Match      68.0%; Score 13.6; DB 12; Length 50;
Best Local Similarity 80.0%; Pred. No. 6.7e+02;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
QY      1 TTATGAATGATACCGTCAT 20
        |||||||
Db      41 TTATGAATGATACCGTCAT 22
```

```
RESULT 13
US-11-175-859-83366
; Sequence 83366, Application US/11/175859
; Publication No. US20060024715A1
; GENERAL INFORMATION:
; APPLICANT: Affymetrix, Inc.
; APPLICANT: Liu, Guoying et al.
; TITLE OF INVENTION: Method of Analysis of Human Polymorphism
; FILE REFERENCE: 3690.1
; CURRENT APPLICATION NUMBER: US/11/175,859
; CURRENT FILING DATE: 2005-07-05
; PRIOR APPLICATION NUMBER: US 60/585,352
; PRIOR FILING DATE: 2004-07-02
; NUMBER OF SEQ ID NOS: 116251
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 83366
; LENGTH: 50
; TYPE: DNA
; ORGANISM: homo sapien
US-11-175-859-83366
```

```
Query Match      68.0%; Score 13.6; DB 12; Length 50;
Best Local Similarity 80.0%; Pred. No. 6.7e+02;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
QY      1 TTATGAATGATACCGTCAT 20
        |||||||
Db      2 TCAATGAATGATACCGTCAT 21
```

```
RESULT 14
US-11-101-244-1019090
```

ORGANISM: Homo sapiens
US-11-101-244-222605

Query Match
Best Local Similarity 80.0%; Score 16; DB 10; Length 19;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTATGGAATGATACCG 16
Db 16 TTATGGAATGATACCG 1

RESULT 5
US-11-083-784-222605/c
; Sequence 222605, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 134990S
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 222605
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-222605

Query Match
Best Local Similarity 100.0%; Score 16; DB 11; Length 19;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTATGGAATGATACCG 16
Db 16 TTATGGAATGATACCG 1

RESULT 6
US-11-121-849-481834/c
; Sequence 481834, Application US/11121849
; Publication No. US2005027080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; TITLE OF INVENTION: Microarrays
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 481834
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-481834

Query Match
Best Local Similarity 71.0%; Score 14.2; DB 12; Length 25;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 TTATGGAATGATACCGTCA 19
Db 25 TCATGGAATGATACCTCA 7

RESULT 7
US-11-121-849-621659
; Sequence 621659, Application US/11121849
; Publication No. US2005027080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded
; TITLE OF INVENTION: Microarrays
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 621659
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-621659

Query Match
Best Local Similarity 71.0%; Score 14.2; DB 12; Length 25;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 TTATGGAATGATACCGTCA 19
Db 6 TTATGGAATGATACCTCA 24

RESULT 8
US-11-175-859-35121
; Sequence 35121, Application US/11175859
; Publication No. US20060024715A1
; GENERAL INFORMATION:
; APPLICANT: Affymetrix, Inc.
; APPLICANT: Liu, Guoying et al.
; TITLE OF INVENTION: Method of Analysis of Human Polymorphism
; FILE REFERENCE: 3630.1
; CURRENT APPLICATION NUMBER: US/11/175,859
; CURRENT FILING DATE: 2005-07-05
; PRIOR APPLICATION NUMBER: US 60/585,352
; PRIOR FILING DATE: 2004-07-02
; NUMBER OF SEQ ID NOS: 116251
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 35121
; LENGTH: 50
; TYPE: DNA
; ORGANISM: homo sapien
US-11-175-859-35121

Query Match
Best Local Similarity 71.0%; Score 14.2; DB 12; Length 50;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 TTATGGAATGATACCGTCA 19
Db 7 TTATGGAATGATACGCTCA 25

RESULT 9
US-11-175-859-31104
; Sequence 31104, Application US/11175859
; Publication No. US20060024715A1
; GENERAL INFORMATION:
; APPLICANT: Affymetrix, Inc.

c 94 12.6 63.0 25 12 US-11-121-849-333296 Sequence 333296,
95 12.6 63.0 25 12 US-11-121-849-341700 Sequence 341700,
96 12.6 63.0 25 12 US-11-121-849-343227 Sequence 343227,
c 97 12.6 63.0 25 12 US-11-121-849-348164 Sequence 348164,
98 12.6 63.0 25 12 US-11-121-849-371845 Sequence 371845,
99 12.6 63.0 25 12 US-11-121-849-440130 Sequence 440130,
c 100 12.6 63.0 25 12 US-11-121-849-550186 Sequence 550186,

ALIGNMENTS

RESULT 1

US-11-101-244-222615/c
; Sequence 222615, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 222615
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-222615

Query Match 90.0%; Score 18; DB 10; Length 19;

Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTATGAATGATACCGTC 18
DB 18 TTATGAATGATACCGTC 1

RESULT 2

US-11-083-784-222615/c
; Sequence 222615, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 222615
; LENGTH: 19

; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-222615

Query Match 90.0%; Score 18; DB 11; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTATGAATGATACCGTC 18
DB 18 TTATGAATGATACCGTC 1

RESULT 3

US-11-024-959-556/c
; Sequence 556, Application US/11024959
; Publication No. US20060010516A1
; GENERAL INFORMATION:
; APPLICANT: FORSTER, RICHARD L.
; APPLICANT: CONNETT, MARIE B.
; APPLICANT: EMERSON, SARAH JANE
; APPLICANT: GRIGOR, MURRAY ROBERT
; APPLICANT: HIGGINS, COLLEEN M.
; APPLICANT: LUND, STEVEN TROY
; APPLICANT: MAGUSIN, ANDREAS
; APPLICANT: KODRZYCKI, BOB
; TITLE OF INVENTION: CELL CYCLE GENES AND RELATED METHODS
; FILE REFERENCE: 044463-0360
; CURRENT APPLICATION NUMBER: US/11/024,959
; CURRENT FILING DATE: 2004-12-30
; PRIOR APPLICATION NUMBER: 60/533,036
; PRIOR FILING DATE: 2003-12-30
; NUMBER OF SEQ ID NOS: 782
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 556
; LENGTH: 60
; TYPE: DNA
; ORGANISM: Eucalyptus sp.
US-11-024-959-556

Query Match 84.0%; Score 16.8; DB 12; Length 60;
Best Local Similarity 90.0%; Pred. No. 11;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TTATGAATGATACCGTCAT 20
DB 44 TTATGAATGATACCGTCAT 25

RESULT 4

US-11-101-244-222605/c
; Sequence 222605, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 222605
; LENGTH: 19
; TYPE: RNA

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: March 1, 2006, 22:45:50 ; Search time 496 Seconds
(without alignments)
88.402 Million cell updates/sec

Title: US-10-653-528-33
Perfect score: 1 ctatggaatcataccgtcat 20
Sequence:

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 7218512 seqs, 1096188070 residues 11869650
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 80

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database :

Published Applications_MA_New:*
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11: /cgn2_6/ptodaca/1/pubpna/US11_NEW_PUB.seq4:*
12: /cgn2_6/ptodaca/1/pubpna/US11_NEW_PUB.seq4:*
13: /cgn2_6/ptodaca/1/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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C 2	18	90.0	19	11	US-11-083-784-222615 Sequence 222615,
C 3	16.8	84.0	60	12	US-11-024-959-556 Sequence 556, App
C 4	16	80.0	19	10	US-11-101-244-222605 Sequence 222605,
C 5	16	80.0	19	11	US-11-083-784-222605 Sequence 222605,
C 6	14.2	71.0	25	12	US-11-121-849-481834 Sequence 481834,
C 7	14.2	71.0	25	12	US-11-121-849-621659 Sequence 621659,
C 8	14.2	71.0	50	12	US-11-175-859-31521 Sequence 31521, A
C 9	13.8	69.0	50	12	US-11-175-859-31104 Sequence 31104, A
C 10	13.8	69.0	50	12	US-11-175-859-108552 Sequence 108552,
C 11	13.6	68.0	25	12	US-11-121-849-550185 Sequence 550185,
C 12	13.6	68.0	50	12	US-11-175-859-48186 Sequence 48186, A
C 13	13.6	68.0	50	12	US-11-175-859-83366 Sequence 83366, A
C 14	13.4	67.0	19	10	US-11-101-244-1019090 Sequence 1019090,
C 15	13.4	67.0	19	11	US-11-083-784-1019090 Sequence 1019090,
C 16	13.4	67.0	25	12	US-11-121-849-649077 Sequence 649077,
C 17	13.4	67.0	25	12	US-11-121-849-649078 Sequence 649078,
C 18	13.4	67.0	25	12	US-11-121-849-649079 Sequence 649079,
C 19	13.4	67.0	25	12	US-11-121-849-649841 Sequence 649841,
C 20	13.4	67.0	25	12	US-11-121-849-649842 Sequence 649842,

C 21	13.4	67.0	25	12	US-11-136-527-26188 Sequence 26188, A
C 22	13.4	67.0	25	12	US-11-136-527-26191 Sequence 26191, A
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C 24	13.4	67.0	25	12	US-11-136-527-293123 Sequence 293123,
C 25	13.4	67.0	50	12	US-11-175-859-30250 Sequence 30250, A
C 26	13.2	66.0	19	10	US-11-101-244-605119 Sequence 605119,
C 27	13.2	66.0	19	10	US-11-101-244-1066281 Sequence 1066281,
C 28	13.2	66.0	19	10	US-11-101-244-1463744 Sequence 1463744,
C 29	13.2	66.0	19	11	US-11-083-784-605119 Sequence 605119,
C 30	13.2	66.0	19	11	US-11-083-784-1066281 Sequence 1066281,
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C 32	13.2	66.0	22	8	US-10-310-914A-371492 Sequence 371492,
C 33	13.2	66.0	25	12	US-11-121-849-315871 Sequence 315871,
C 34	13.2	66.0	25	12	US-11-121-849-315872 Sequence 315872,
C 35	13.2	66.0	25	12	US-11-121-849-594174 Sequence 594174,
C 36	13.2	66.0	25	12	US-11-136-527-130457 Sequence 130457,
C 37	13.2	66.0	25	12	US-11-136-527-130458 Sequence 130458,
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C 39	13.2	66.0	25	12	US-11-136-527-130471 Sequence 130471,
C 40	13.2	66.0	25	12	US-11-136-527-130474 Sequence 130474,
C 41	13.2	66.0	25	12	US-11-136-527-130479 Sequence 130479,
C 42	13.2	66.0	25	12	US-11-136-527-130480 Sequence 130480,
C 43	13.2	66.0	25	12	US-11-136-527-334264 Sequence 334264,
C 44	13.2	66.0	30	8	US-10-857-780-411 Sequence 411, App
C 45	13.2	66.0	50	12	US-11-175-859-22870 Sequence 22870, A
C 46	13.2	66.0	50	12	US-11-175-859-25539 Sequence 25539, A
C 47	13.2	66.0	50	12	US-11-175-859-26397 Sequence 26397, A
C 48	13.2	66.0	50	12	US-11-175-859-45246 Sequence 45246, A
C 49	13.2	66.0	50	12	US-11-175-859-53781 Sequence 53781, A
C 50	13.2	66.0	50	12	US-11-175-859-55867 Sequence 55867, A
C 51	13.2	66.0	50	12	US-11-175-859-57813 Sequence 57813, A
C 52	13.2	66.0	70	8	US-10-310-914A-11787 Sequence 11787, A
C 53	13	65.0	30	4	US-10-310-914A-62324 Sequence 62324, A
C 54	13	65.0	50	12	US-11-175-859-73443 Sequence 73443, A
C 55	13	65.0	50	12	US-11-175-859-86140 Sequence 86140, A
C 56	12.8	64.0	18	8	US-10-310-914A-55166 Sequence 55166, A
C 57	12.8	64.0	19	10	US-11-101-244-21012 Sequence 21012, A
C 58	12.8	64.0	19	10	US-11-101-244-21031 Sequence 21031, A
C 59	12.8	64.0	19	10	US-11-101-244-352271 Sequence 352271,
C 60	12.8	64.0	19	10	US-11-101-244-476003 Sequence 476003,
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C 67	12.8	64.0	21	8	US-10-310-914A-55270 Sequence 55270, A
C 68	12.8	64.0	21	8	US-10-310-914A-87008 Sequence 87008, A
C 69	12.8	64.0	22	8	US-10-310-914A-1090094 Sequence 1090094,
C 70	12.8	64.0	25	12	US-11-121-849-359930 Sequence 359930,
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C 72	12.8	64.0	25	12	US-11-121-849-585552 Sequence 585552,
C 73	12.8	64.0	25	12	US-11-121-849-585553 Sequence 585553,
C 74	12.8	64.0	25	12	US-11-136-527-286565 Sequence 286565,
C 75	12.8	64.0	50	12	US-11-175-859-12183 Sequence 12183, A
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C 77	12.8	64.0	50	12	US-11-175-859-87519 Sequence 87519, A
C 78	12.8	64.0	50	12	US-11-175-859-100942 Sequence 100942,
C 79	12.6	63.0	19	10	US-11-101-244-222527 Sequence 222527,
C 80	12.6	63.0	19	10	US-11-101-244-1044820 Sequence 1044820,
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C 82	12.6	63.0	21	8	US-11-083-784-1044820 Sequence 1044820,
C 83	12.6	63.0	21	8	US-10-671-740-158 Sequence 158, App
C 84	12.6	63.0	23	8	US-10-310-914A-394101 Sequence 394101,
C 85	12.6	63.0	23	8	US-10-310-914A-643439 Sequence 643439,
C 86	12.6	63.0	24	8	US-10-310-914A-761640 Sequence 761640,
C 87	12.6	63.0	24	8	US-10-310-914A-472122 Sequence 472122,
C 88	12.6	63.0	25	8	US-10-995-561-85159 Sequence 85159, A
C 89	12.6	63.0	25	8	US-10-995-561-85162 Sequence 85162, A
C 90	12.6	63.0	25	12	US-11-121-849-55287 Sequence 55287, A
C 91	12.6	63.0	25	12	US-11-121-849-69047 Sequence 69047, A
C 92	12.6	63.0	25	12	US-11-121-849-96196 Sequence 96196, A
C 93	12.6	63.0	25	12	US-11-121-849-309834 Sequence 309834,

Db 80 ATGGAATTATATCGTCA 64

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RESULT 28
US-11-033-489-38/c
; Sequence 38, Application US/11033489
; Publication No. US20050182243A1
; GENERAL INFORMATION:
; APPLICANT: Sligar, Stephen G
; APPLICANT: Baybutt, Timothy H
; APPLICANT: Schuler, Mary A
; APPLICANT: Civan, Nataraya R
; APPLICANT: Grinkova, Yelena V.
; APPLICANT: Denisov, Ilya G.
; APPLICANT: Grime, Stephen G.
; TITLE OF INVENTION: Membrane Scaffold Proteins
; FILE REFERENCE: 87-00B
; CURRENT APPLICATION NUMBER: US/11/033,489
; CURRENT FILING DATE: 2005-01-11
; PRIOR APPLICATION NUMBER: 09/990,087
; PRIOR FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: 10/465,789
; PRIOR FILING DATE: 2003-06-18
; PRIOR APPLICATION NUMBER: 60/536,281
; PRIOR FILING DATE: 2004-01-13
; PRIOR APPLICATION NUMBER: 60/252,233
; PRIOR FILING DATE: 2000-11-20
; NUMBER OF SEQ ID NOS: 136
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 38
; LENGTH: 80
; TYPE: DNA
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: synthetic oligonucleotide
US-11-033-489-38

Query Match 69.0%; Score 13.8; DB 10; Length 80;
Best Local Similarity 88.2%; Pred. No. 6.6e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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QY 3 ATGGAATGATACCGTCA 19
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Db 80 ATGGAATTATATCGTCA 64

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RESULT 29
US-10-719-900-606555/c
; Sequence 606555, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 606555
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-606555
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Query Match 68.0%; Score 13.6; DB 8; Length 25;
Best Local Similarity 80.0%; Pred. No. 7e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 TTATGGAATGATACCGTCA 20
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Db 22 TTAGGAATGATACCTGAAT 3

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RESULT 30
US-10-956-157-211298/c
; Sequence 211298, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 211298
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-211298
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Best Local Similarity 80.0%; Pred. No. 7e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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Job time : 619.333 secs

US-11-033-489-65
; Sequence 65, Application US/11033489
; Publication No. US20050182243A1
; GENERAL INFORMATION:
; APPLICANT: Sligar, Stephen G
; APPLICANT: Bayburt, Timothy H
; APPLICANT: Schuler, Mary A
; APPLICANT: Civan, Natanya R
; APPLICANT: Grinkova, Yelena V.
; APPLICANT: Denisov, Ilya G.
; APPLICANT: Grimme, Stephen G.
; TITLE OF INVENTION: Membrane Scaffold Proteins
; FILE REFERENCE: 87-00B
; CURRENT APPLICATION NUMBER: US/11/033,489
; CURRENT FILING DATE: 2005-01-11
; PRIOR APPLICATION NUMBER: 09/990,087
; PRIOR FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: 10/465,789
; PRIOR FILING DATE: 2003-06-18
; PRIOR APPLICATION NUMBER: 60/536,281
; PRIOR FILING DATE: 2004-01-13
; PRIOR APPLICATION NUMBER: 60/252,233
; PRIOR FILING DATE: 2000-11-20
; NUMBER OF SEQ ID NOS: 136
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 65
; LENGTH: 66
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: sequence encoding Helix 4
US-11-033-489-65

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Best Local Similarity 88.2%; Pred. No. 6.4e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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DB 40 ATGAATTATATCGTCA 56

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; Sequence 47, Application US/10448250
; Publication No. US20040018530A1
; GENERAL INFORMATION:
; APPLICANT: Bowser, Michael T
; APPLICANT: Wendonsa, Shaun D
; TITLE OF INVENTION: IN VITRO EVOLUTION OF FUNCTIONAL RNA AND DNA USING
; FILE REFERENCE: 110.01870101
; CURRENT APPLICATION NUMBER: US/10/448,250
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: 60/384,709
; PRIOR FILING DATE: 2002-05-31
; PRIOR APPLICATION NUMBER: 60/470,750
; PRIOR FILING DATE: 2003-05-15
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 47
; LENGTH: 80
; TYPE: DNA
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: aptamer
US-10-448-250-47

Query Match 69.0%; Score 13.8; DB 7; Length 80;
Best Local Similarity 88.2%; Pred. No. 6.6e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 TGAATGATACCGTCA 20

DB 34 TGAATGATACCGTCA 18

RESULT 26
US-10-465-789A-38/c
; Sequence 38, Application US/10465789A
; Publication No. US2004005384A1
; GENERAL INFORMATION:
; APPLICANT: Sligar, Stephen G
; APPLICANT: Bayburt, Timothy H
; APPLICANT: Schuler, Mary A
; APPLICANT: Civan, Natanya R
; APPLICANT: Grinkova, Yelena V.
; APPLICANT: Denisov, Ilya G.
; TITLE OF INVENTION: Membrane Scaffold Proteins
; FILE REFERENCE: 87-00A
; CURRENT APPLICATION NUMBER: US/10/465,789A
; CURRENT FILING DATE: 2003-06-18
; PRIOR APPLICATION NUMBER: 09/990,087
; PRIOR FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: 60/252,233
; PRIOR FILING DATE: 2000-11-20
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 38
; LENGTH: 80
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic oligonucleotide
US-10-465-789A-38

Query Match 69.0%; Score 13.8; DB 7; Length 80;
Best Local Similarity 88.2%; Pred. No. 6.6e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 ATGAATGATACCGTCA 19
DB 80 ATGAATTATATCGTCA 64

RESULT 27
US-10-979-506-38/c
; Sequence 38, Application US/10979506
; Publication No. US20050152984A1
; GENERAL INFORMATION:
; APPLICANT: Sligar, Stephen G
; APPLICANT: Bayburt, Timothy H
; TITLE OF INVENTION: Membrane Scaffold Proteins
; FILE REFERENCE: 87-00C
; CURRENT APPLICATION NUMBER: US/10/979,506
; CURRENT FILING DATE: 2004-11-02
; PRIOR APPLICATION NUMBER: 09/990,087
; PRIOR FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: 60/252,233
; PRIOR FILING DATE: 2000-11-20
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 38
; LENGTH: 80
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic oligonucleotide
US-10-979-506-38

Query Match 69.0%; Score 13.8; DB 9; Length 80;
Best Local Similarity 88.2%; Pred. No. 6.6e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 ATGAATGATACCGTCA 19

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APPLICANT: Civjan, Natanya R
APPLICANT: Yelena V. Grinkova
APPLICANT: Ilya G. Denisov
TITLE OF INVENTION: Membrane Scaffold Proteins
FILE REFERENCE: 87-00A
CURRENT APPLICATION NUMBER: US/10/465,789A
CURRENT FILING DATE: 2003-06-18
PRIOR APPLICATION NUMBER: 09/990,087
PRIOR FILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: 60/252,233
PRIOR FILING DATE: 2000-11-20
NUMBER OF SEQ ID NOS: 89
SOFTWARE: PatentIn version 3.1
SEQ ID NO 32
LENGTH: 54
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: synthetic oligonucleotide
US-10-465-789A-32
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Query Match      69.0%; Score 13.8; DB 7; Length 54;
Best Local Similarity 88.2%; Pred. No. 6.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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DB      37 ATGGAATTATATCGTCA 53
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RESULT 21
US-10-979-506-32
; Sequence 32, Application US/10979506
; Publication No. US20050152984A1
; GENERAL INFORMATION:
; APPLICANT: Sligar, Stephen G
; APPLICANT: Bayburt, Timothy H
; TITLE OF INVENTION: Membrane Scaffold Proteins
; FILE REFERENCE: 87-00C
; CURRENT APPLICATION NUMBER: US/10/979,506
; CURRENT FILING DATE: 2004-11-02
; PRIOR APPLICATION NUMBER: 09/990,087
; PRIOR FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: 60/252,233
; PRIOR FILING DATE: 2000-11-20
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 32
; LENGTH: 54
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic oligonucleotide
US-10-979-506-32
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Query Match      69.0%; Score 13.8; DB 9; Length 54;
Best Local Similarity 88.2%; Pred. No. 6.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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DB      37 ATGGAATTATATCGTCA 53
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RESULT 22
US-11-033-489-32
; Sequence 32, Application US/11033489
; Publication No. US20050182243A1
; GENERAL INFORMATION:
; APPLICANT: Sligar, Stephen G
; APPLICANT: Bayburt, Timothy H
; APPLICANT: Schuler, Mary A
; APPLICANT: Civjan, Natanya R
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APPLICANT: Grinkova, Yelena V.
APPLICANT: Denisov, Ilya G.
APPLICANT: Grime, Stephen G.
TITLE OF INVENTION: Membrane Scaffold Proteins
FILE REFERENCE: 87-00B
CURRENT APPLICATION NUMBER: US/11/033,489
CURRENT FILING DATE: 2005-01-11
PRIOR APPLICATION NUMBER: 09/990,087
PRIOR FILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: 10/465,789
PRIOR FILING DATE: 2003-06-18
PRIOR APPLICATION NUMBER: 60/536,281
PRIOR FILING DATE: 2004-01-13
PRIOR APPLICATION NUMBER: 60/252,233
PRIOR FILING DATE: 2000-11-20
NUMBER OF SEQ ID NOS: 136
SOFTWARE: PatentIn version 3.3
SEQ ID NO 32
LENGTH: 54
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: synthetic oligonucleotide
US-11-033-489-32
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Query Match      69.0%; Score 13.8; DB 10; Length 54;
Best Local Similarity 88.2%; Pred. No. 6.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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DB      37 ATGGAATTATATCGTCA 53
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RESULT 23
US-10-465-789A-65
; Sequence 65, Application US/10465789A
; Publication No. US20040053384A1
; GENERAL INFORMATION:
; APPLICANT: Sligar, Stephen G
; APPLICANT: Bayburt, Timothy H
; APPLICANT: Schuler, Mary A
; APPLICANT: Civjan, Natanya R
; APPLICANT: Yelena V. Grinkova
; APPLICANT: Ilya G. Denisov
; TITLE OF INVENTION: Membrane Scaffold Proteins
; FILE REFERENCE: 87-00A
; CURRENT APPLICATION NUMBER: US/10/465,789A
; CURRENT FILING DATE: 2003-06-18
; PRIOR APPLICATION NUMBER: 09/990,087
; PRIOR FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: 60/252,233
; PRIOR FILING DATE: 2000-11-20
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 65
; LENGTH: 66
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: sequence encoding Helix 4
US-10-465-789A-65
```

```
Query Match      69.0%; Score 13.8; DB 7; Length 66;
Best Local Similarity 88.2%; Pred. No. 6.4e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      3 ATGGAATGATACCGTCA 19
      ||||| ||||| |||||
DB      40 ATGGAATTATATCGTCA 56
```

RESULT 24

```

; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 275339
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-275339

```

```

Query Match          69.0%; Score 13.8; DB 8; Length 25;
Best Local Similarity 88.2%; Pred. No. 5.6e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      3 ATGGAATGATACCGTCA 19
DB      19 ATGGAATGATACGTTA 3

```

```

RESULT 16
US-10-719-900-744113/C
; Sequence 744113, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 744113
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-744113

```

```

Query Match          69.0%; Score 13.8; DB 8; Length 25;
Best Local Similarity 88.2%; Pred. No. 5.6e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      4 TGGATGATACCGCAT 20
DB      20 TGGACTGATACCGCTT 4

```

```

RESULT 17
US-11-036-317-473162/C
; Sequence 473162, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 473162
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-473162

```

```

Query Match          69.0%; Score 13.8; DB 10; Length 25;
Best Local Similarity 88.2%; Pred. No. 5.6e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2 TATGATGATACCGTTC 18
DB      25 TTTGATGATACCGTTC 9

```

```

RESULT 18
US-11-036-317-985351
; Sequence 985351, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 985351
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-985351

```

```

Query Match          69.0%; Score 13.8; DB 10; Length 25;
Best Local Similarity 88.2%; Pred. No. 5.6e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 TTATGATGATACCGT 17
DB      1 TTATGGATGATAACCGT 17

```

```

RESULT 19
US-10-784-880-328
; Sequence 328, Application US/10784880
; Publication No. US20040208890A1
; GENERAL INFORMATION:
; APPLICANT: SUBTIL-SANDS, AGATHE
; APPLICANT: DAUTRY-VARSA, ALICE
; TITLE OF INVENTION: SECRETED CHLAMYDIA POLYPEPTIDES, POLYNUCLEOTIDES CODING THEREOF
; FILE REFERENCE: 249179US0
; CURRENT APPLICATION NUMBER: US/10/784,880
; CURRENT FILING DATE: 2004-02-24
; PRIOR APPLICATION NUMBER: US 60/448,879
; PRIOR FILING DATE: 2003-02-24
; NUMBER OF SEQ ID NOS: 378
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 328
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic DNA
US-10-784-880-328

```

```

Query Match          69.0%; Score 13.8; DB 8; Length 30;
Best Local Similarity 88.2%; Pred. No. 5.7e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      3 ATGATGATACCGTCA 19
DB      10 ATGCAATGATATCGTCA 26

```

```

RESULT 20
US-10-465-789A-32
; Sequence 32, Application US/10465789A
; Publication No. US20040053384A1
; GENERAL INFORMATION:
; APPLICANT: Sligar, Stephen G
; APPLICANT: Baybutt, Timothy H
; APPLICANT: Schuler, Mary A

```

;; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
;; SEQ ID NO 72805
;; LENGTH: 25
;; TYPE: DNA
;; ORGANISM: Rattus norvegicus
US-10-719-956-72805

Query Match 72.0%; Score 14.4; DB 7; Length 25;
Best Local Similarity 93.8%; Pred. No. 2.7e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 GGATGATACCGTCAT 20
Db 10 GGATGATACCGTCAT 25

RESULT 11

US-10-719-900-612502/c
;; Sequence 612502, Application US/10719900
;; Publication No. US20050026164A1
;; GENERAL INFORMATION:
;; APPLICANT: Xue Mei Zhou
;; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
;; FILE REFERENCE: 3528.1
;; CURRENT APPLICATION NUMBER: US/10/719,900
;; CURRENT FILING DATE: 2003-11-20
;; PRIOR APPLICATION NUMBER: 60/427,808
;; PRIOR FILING DATE: 2002 11 20
;; NUMBER OF SEQ ID NOS: 982914
;; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
;; SEQ ID NO 612502
;; LENGTH: 25
;; TYPE: DNA
;; ORGANISM: Mus musculus
US-10-719-900-612502

Query Match 72.0%; Score 14.4; DB 8; Length 25;
Best Local Similarity 93.8%; Pred. No. 2.7e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TATGATGATACCGTC 17
Db 21 TCTGATGATACCGTC 6

RESULT 12

US-11-036-317-494473
;; Sequence 494473, Application US/11036317
;; Publication No. US20050214823A1
;; GENERAL INFORMATION:
;; APPLICANT: Williams, Alan
;; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
;; FILE REFERENCE: 3654.1
;; CURRENT APPLICATION NUMBER: US/11/036,317
;; CURRENT FILING DATE: 2005-01-13
;; PRIOR APPLICATION NUMBER: US 60/536,639
;; PRIOR FILING DATE: 2004-01-13
;; NUMBER OF SEQ ID NOS: 991174
;; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
;; SEQ ID NO 494473
;; LENGTH: 25
;; TYPE: DNA
;; ORGANISM: Mus musculus
US-11-036-317-494473

Query Match 71.0%; Score 14.2; DB 10; Length 25;
Best Local Similarity 84.2%; Pred. No. 3.5e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 TTATGATGATACCGTC 19
Db 3 TCATGATGATACCGTC 21

RESULT 13

US-10-719-956-313188/c
;; Sequence 313188, Application US/10719956
;; Publication No. US20040146910A1
;; GENERAL INFORMATION:
;; APPLICANT: Xue Mei Zhou
;; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
;; FILE REFERENCE: 3527.1
;; CURRENT APPLICATION NUMBER: US/10/719,956
;; CURRENT FILING DATE: 2003-11-20
;; PRIOR APPLICATION NUMBER: 60/427,836
;; PRIOR FILING DATE: 2002 11 20
;; NUMBER OF SEQ ID NOS: 699466
;; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
;; SEQ ID NO 313188
;; LENGTH: 25
;; TYPE: DNA
;; ORGANISM: Rattus norvegicus
US-10-719-956-313188

Query Match 69.0%; Score 13.8; DB 7; Length 25;
Best Local Similarity 88.2%; Pred. No. 5.6e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 TGGATGATACCGTCAT 20
Db 25 TTGATGATACCGTCAT 9

RESULT 14

US-10-719-900-263303/c
;; Sequence 263303, Application US/10719900
;; Publication No. US20050026164A1
;; GENERAL INFORMATION:
;; APPLICANT: Xue Mei Zhou
;; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
;; FILE REFERENCE: 3528.1
;; CURRENT APPLICATION NUMBER: US/10/719,900
;; CURRENT FILING DATE: 2003-11-20
;; PRIOR APPLICATION NUMBER: 60/427,808
;; PRIOR FILING DATE: 2002 11 20
;; NUMBER OF SEQ ID NOS: 982914
;; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
;; SEQ ID NO 263303
;; LENGTH: 25
;; TYPE: DNA
;; ORGANISM: Mus musculus
US-10-719-900-263303

Query Match 69.0%; Score 13.8; DB 8; Length 25;
Best Local Similarity 88.2%; Pred. No. 5.6e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TATGATGATACCGTC 18
Db 20 TATGATGATACCGTC 4

RESULT 15

US-10-719-900-275339/c
;; Sequence 275339, Application US/10719900
;; Publication No. US20050026164A1
;; GENERAL INFORMATION:
;; APPLICANT: Xue Mei Zhou
;; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
;; FILE REFERENCE: 3528.1
;; CURRENT APPLICATION NUMBER: US/10/719,900
;; CURRENT FILING DATE: 2003-11-20
;; PRIOR APPLICATION NUMBER: 60/427,808
;; PRIOR FILING DATE: 2002 11 20
;; NUMBER OF SEQ ID NOS: 982914

Query Match 95.0%; Score 19; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TATGGAATGATACCGTCAT 20
DB 1 TATGGAATGATACCGTCAT 19

RESULT 6

US-10-653-528-34
; Sequence 34, Application US/10653528
; Publication No. US2004007578A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 2 EXPRESSION
; FILE REFERENCE: PFS-0022
; CURRENT APPLICATION NUMBER: US/10/653,528
; CURRENT FILING DATE: 2003-09-02
; PRIOR APPLICATION NUMBER: US/10/173,192
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 71
; SEQ ID NO 34
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-653-528-34

Query Match 95.0%; Score 19; DB 7; Length 20;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TATGGAATGATACCGTCAT 20
DB 1 TATGGAATGATACCGTCAT 19

RESULT 7

US-10-745-242A-31/c
; Sequence 31, Application US/10745242A
; Publication No. US2004019788BA1
; GENERAL INFORMATION:
; APPLICANT: Armour, Christopher D
; APPLICANT: Loerch, Patrick
; APPLICANT: Castle, John C
; APPLICANT: Johnson, Jason M
; TITLE OF INVENTION: Alternatively Spliced Isoforms of Histone Deacetylase 3 (HDAC3)
; FILE REFERENCE: RS0207Y
; CURRENT APPLICATION NUMBER: US/10/745,242A
; CURRENT FILING DATE: 2003-12-22
; PRIOR APPLICATION NUMBER: US 60/437,666
; PRIOR FILING DATE: 2002-12-31
; PRIOR APPLICATION NUMBER: US 60/478,233
; PRIOR FILING DATE: 2003-06-12
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 31
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-745-242A-31

Query Match 76.0%; Score 15.2; DB 8; Length 20;
Best Local Similarity 85.0%; Pred. No. 1e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TTATGGAATGATACCGTCAT 20
DB 20 TTGTGGAAGGACACCGTCAT 1

RESULT 8

US-10-956-157-296567/c
; Sequence 296567, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounes, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WI
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 296567
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-296567

Query Match 76.0%; Score 15.2; DB 9; Length 25;
Best Local Similarity 85.0%; Pred. No. 1.1e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TTATGGAATGATACCGTCAT 20
DB 22 TTGTGGAAGGACACCGTCAT 3

RESULT 9

US-10-956-157-296568/c
; Sequence 296568, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounes, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WI
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 296568
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-296568

Query Match 76.0%; Score 15.2; DB 9; Length 25;
Best Local Similarity 85.0%; Pred. No. 1.1e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TTATGGAATGATACCGTCAT 20
DB 22 TTGTGGAAGGACACCGTCAT 3

RESULT 10

US-10-719-956-72805
; Sequence 72805, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466

C 97 12.8 64.0 25 10 US-11-036-317-537788 Sequence 537788,
C 98 12.8 64.0 25 10 US-11-060-756-54930 Sequence 54930, A
C 99 12.8 64.0 25 10 US-11-060-756-54942 Sequence 54942, A
C 100 12.8 64.0 25 10 US-11-060-756-54943 Sequence 54943, A

ALIGNMENTS

RESULT 1
US-10-173-192-33

Sequence 33, Application US/10173192
Publication No. US20030236204A1

GENERAL INFORMATION:

APPLICANT: Kenneth W. Dobie

TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 2 EXPRESSION

FILE REFERENCE: PTS-0022

CURRENT APPLICATION NUMBER: US/10/173,192

CURRENT FILING DATE: 2002-06-14

NUMBER OF SEQ ID NOS: 71

SEQ ID NO 33

LENGTH: 20

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Antisense Oligonucleotide

US-10-173-192-33

Query Match Best Local Similarity 100.0%; Score 20; DB 6; Length 20;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTATGAATGATACCGTCAT 20
Db 1 TTATGAATGATACCGTCAT 20

RESULT 2

US-10-173-192-61/c

Sequence 61, Application US/10173192
Publication No. US20030236204A1

GENERAL INFORMATION:

APPLICANT: Kenneth W. Dobie

TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 2 EXPRESSION

FILE REFERENCE: PTS-0022

CURRENT APPLICATION NUMBER: US/10/173,192

CURRENT FILING DATE: 2002-06-14

NUMBER OF SEQ ID NOS: 71

SEQ ID NO 61

LENGTH: 20

TYPE: DNA

ORGANISM: H. sapiens

FEATURE:

US-10-173-192-61

Query Match Best Local Similarity 100.0%; Score 20; DB 6; Length 20;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTATGAATGATACCGTCAT 20
Db 20 TTATGAATGATACCGTCAT 1

RESULT 3

US-10-653-528-33

Sequence 33, Application US/10653528
Publication No. US20040077578A1

GENERAL INFORMATION:

APPLICANT: Brett P. Monia

APPLICANT: Kenneth W. Dobie

TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 2 EXPRESSION

FILE REFERENCE: PTS-0022

CURRENT APPLICATION NUMBER: US/10/653,528

CURRENT FILING DATE: 2003-09-02

PRIOR APPLICATION NUMBER: US/10/173,192

PRIOR FILING DATE: 2002-06-14

NUMBER OF SEQ ID NOS: 71

SEQ ID NO 33

LENGTH: 20

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Antisense Oligonucleotide

US-10-653-528-33

Query Match Best Local Similarity 100.0%; Score 20; DB 7; Length 20;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTATGAATGATACCGTCAT 20
Db 1 TTATGAATGATACCGTCAT 20

RESULT 4

US-10-653-528-61/c

Sequence 61, Application US/10653528
Publication No. US20040077578A1

GENERAL INFORMATION:

APPLICANT: Kenneth W. Dobie

TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 2 EXPRESSION

FILE REFERENCE: PTS-0022

CURRENT APPLICATION NUMBER: US/10/653,528

CURRENT FILING DATE: 2003-09-02

PRIOR APPLICATION NUMBER: US/10/173,192

PRIOR FILING DATE: 2002-06-14

NUMBER OF SEQ ID NOS: 71

SEQ ID NO 61

LENGTH: 20

TYPE: DNA

ORGANISM: H. sapiens

FEATURE:

US-10-653-528-61

Query Match Best Local Similarity 100.0%; Score 20; DB 7; Length 20;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTATGAATGATACCGTCAT 20
Db 20 TTATGAATGATACCGTCAT 1

RESULT 5

US-10-173-192-34

Sequence 34, Application US/10173192
Publication No. US20030236204A1

GENERAL INFORMATION:

APPLICANT: Kenneth W. Dobie

TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 2 EXPRESSION

FILE REFERENCE: PTS-0022

CURRENT APPLICATION NUMBER: US/10/173,192

CURRENT FILING DATE: 2002-06-14

NUMBER OF SEQ ID NOS: 71

SEQ ID NO 34

LENGTH: 20

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Antisense Oligonucleotide

US-10-173-192-34

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: March 1, 2006, 22:34:29 ; Search time 617.333 Seconds

(without alignments)
267.906 Million cell updates/sec

Title: US-10-653-528-33

Perfect score: 1 ttaatgaatgataccgcatc 20

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 11282798

Minimum DB seq length: 0
Maximum DB seq length: 80Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : Published Applications_NA_Main:*
1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
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9: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	20	6	US-10-173-192-33 Sequence 33, Appl
2	20	100.0	20	6	US-10-173-192-61 Sequence 61, Appl
3	20	100.0	20	7	US-10-653-528-33 Sequence 33, Appl
4	20	100.0	20	7	US-10-653-528-61 Sequence 61, Appl
5	19	95.0	20	6	US-10-173-192-34 Sequence 34, Appl
6	19	95.0	20	7	US-10-653-528-34 Sequence 34, Appl
7	15.2	76.0	20	8	US-10-745-242A-31 Sequence 31, Appl
8	15.2	76.0	25	9	US-10-956-157-296567 Sequence 296567, Appl
9	15.2	76.0	25	9	US-10-956-157-296568 Sequence 296568, Appl
10	14.4	72.0	25	7	US-10-719-956-72805 Sequence 72805, A
11	14.4	72.0	25	8	US-10-719-956-72806 Sequence 72806, A
12	14.2	71.0	25	10	US-11-036-317-494473 Sequence 494473, A
13	13.8	69.0	25	7	US-10-719-956-313188 Sequence 612502, A
14	13.8	69.0	25	8	US-10-719-956-313189 Sequence 612503, A
15	13.8	69.0	25	8	US-10-719-956-313190 Sequence 612504, A
16	13.8	69.0	25	8	US-10-719-956-313191 Sequence 612505, A
17	13.8	69.0	25	8	US-10-719-956-313192 Sequence 612506, A
18	13.8	69.0	25	8	US-10-719-956-313193 Sequence 612507, A
19	13.8	69.0	30	8	US-10-784-880-328 Sequence 4733162, A
20	13.8	69.0	30	8	US-10-784-880-329 Sequence 4733163, A
21	13.8	69.0	54	9	US-10-979-506-32 Sequence 328, App
22	13.8	69.0	54	9	US-10-979-506-33 Sequence 32, Appl
23	13.8	69.0	54	10	US-11-033-489-32 Sequence 32, Appl
			66	7	US-10-465-789A-65 Sequence 65, Appl

24	13.8	69.0	66	10	US-11-033-489-65 Sequence 65, Appl
25	13.8	69.0	80	7	US-10-448-250-47 Sequence 47, Appl
26	13.8	69.0	80	7	US-10-465-789A-38 Sequence 38, Appl
27	13.8	69.0	80	9	US-10-979-506-38 Sequence 38, Appl
28	13.8	69.0	80	10	US-11-033-489-38 Sequence 38, Appl
29	13.6	68.0	25	8	US-10-719-956-606555 Sequence 606555, A
30	13.6	68.0	25	9	US-10-956-157-211298 Sequence 211298, A
31	13.6	68.0	25	10	US-11-036-317-813617 Sequence 813617, A
32	13.6	68.0	47	6	US-10-349-143-1662 Sequence 1662, Ap
33	13.6	68.0	50	6	US-10-131-827-3668 Sequence 3668, Ap
34	13.6	68.0	55	6	US-10-032-585-3166 Sequence 3166, Ap
35	13.6	68.0	70	9	US-10-957-432-645 Sequence 645, App
36	13.4	67.0	25	8	US-10-719-956-114407 Sequence 114407, A
37	13.4	67.0	25	8	US-10-719-956-671254 Sequence 671254, A
38	13.2	66.0	25	5	US-10-098-2638-25990 Sequence 25990, A
39	13.2	66.0	25	7	US-10-681-773-16187 Sequence 16187, A
40	13.2	66.0	25	7	US-10-681-773-52437 Sequence 52437, A
41	13.2	66.0	25	7	US-10-719-956-527756 Sequence 527756, A
42	13.2	66.0	25	7	US-10-719-956-635934 Sequence 635934, A
43	13.2	66.0	25	7	US-10-719-956-635934 Sequence 635934, A
44	13.2	66.0	25	8	US-10-719-956-439322 Sequence 439322, A
45	13.2	66.0	25	8	US-10-719-956-439322 Sequence 439323, A
46	13.2	66.0	25	8	US-10-719-956-628441 Sequence 628441, A
47	13.2	66.0	25	8	US-10-719-956-671254 Sequence 671254, A
48	13.2	66.0	25	8	US-10-719-956-697939 Sequence 697939, A
49	13.2	66.0	25	8	US-10-719-956-698489 Sequence 698489, A
50	13.2	66.0	25	8	US-10-719-956-704558 Sequence 704558, A
51	13.2	66.0	25	9	US-10-809-189-15329 Sequence 15329, A
52	13.2	66.0	25	9	US-10-809-189-18885 Sequence 18885, A
53	13.2	66.0	25	9	US-10-809-189-18886 Sequence 18886, A
54	13.2	66.0	25	9	US-10-809-189-18886 Sequence 18886, A
55	13.2	66.0	25	9	US-10-956-157-133567 Sequence 133567, A
56	13.2	66.0	25	9	US-10-843-527-75317 Sequence 75317, A
57	13.2	66.0	25	9	US-10-843-527-76296 Sequence 76296, A
58	13.2	66.0	25	9	US-10-843-527-161881 Sequence 161881, A
59	13.2	66.0	25	10	US-11-036-317-482085 Sequence 482085, A
60	13.2	66.0	25	10	US-11-036-317-591364 Sequence 591364, A
61	13.2	66.0	25	10	US-11-036-317-663342 Sequence 663342, A
62	13.2	66.0	25	10	US-11-036-317-663343 Sequence 663343, A
63	13.2	66.0	25	10	US-11-036-317-706070 Sequence 706070, A
64	13.2	66.0	25	10	US-11-036-317-813037 Sequence 813037, A
65	13.2	66.0	25	10	US-11-036-317-828284 Sequence 828284, A
66	13.2	66.0	26	7	US-10-321-039-655 Sequence 655, App
67	13.2	66.0	26	7	US-10-321-039-693 Sequence 693, App
68	13.2	66.0	41	7	US-10-035-833A-4375 Sequence 4375, Ap
69	13.2	66.0	50	6	US-10-131-827-3115 Sequence 3115, Ap
70	13.2	66.0	50	6	US-10-131-827-7377 Sequence 7377, Ap
71	13.2	66.0	60	3	US-09-908-975-8391 Sequence 8391, Ap
72	13.2	66.0	60	3	US-09-908-975-17126 Sequence 17126, A
73	13.2	66.0	60	3	US-09-908-975-21224 Sequence 21224, A
74	13.2	66.0	60	9	US-10-764-420-2868 Sequence 2868, Ap
75	13.2	66.0	25	7	US-10-719-956-71663 Sequence 71663, A
76	13.2	66.0	25	8	US-10-719-956-512579 Sequence 512579, A
77	13.2	66.0	25	10	US-11-060-756-49581 Sequence 49581, A
78	13.2	66.0	25	10	US-11-060-756-49586 Sequence 49586, A
79	13.2	66.0	25	10	US-11-060-756-49608 Sequence 49608, A
80	13.2	66.0	25	10	US-11-060-756-198044 Sequence 198044, A
81	12.8	64.0	25	5	US-10-098-2638-103924 Sequence 103924, A
82	12.8	64.0	25	7	US-10-168-846-56 Sequence 56, Appl
83	12.8	64.0	25	7	US-10-719-956-72806 Sequence 72806, A
84	12.8	64.0	25	7	US-10-719-956-162225 Sequence 162225, A
85	12.8	64.0	25	7	US-10-719-956-222031 Sequence 222031, A
86	12.8	64.0	25	7	US-10-719-956-222031 Sequence 222031, A
87	12.8	64.0	25	7	US-10-719-956-364638 Sequence 364638, A
88	12.8	64.0	25	7	US-10-719-956-628624 Sequence 628624, A
89	12.8	64.0	25	8	US-10-719-956-166445 Sequence 166445, A
90	12.8	64.0	25	8	US-10-719-956-198693 Sequence 198693, A
91	12.8	64.0	25	8	US-10-719-956-535142 Sequence 535142, A
92	12.8	64.0	25	8	US-10-719-956-612503 Sequence 612503, A
93	12.8	64.0	25	8	US-10-719-956-612503 Sequence 612503, A
94	12.8	64.0	25	9	US-10-809-189-75543 Sequence 75543, A
95	12.8	64.0	25	10	US-11-036-317-66072 Sequence 66072, A
96	12.8	64.0	25	10	US-11-036-317-129970 Sequence 129970, A

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/859,998
FILING DATE: 21-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: Field, Bret E.
REGISTRATION NUMBER: 37,620
REFERENCE/DOCKET NUMBER: 09096/002001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-322-5070
TELEFAX: 415-854-0875
INFORMATION FOR SEQ ID NO: 765:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
OTHER INFORMATION: oligonucleotide primer
SEQUENCE DESCRIPTION: SEQ ID NO: 765:
US-09-225-2018-765
Query Match 61.0% Score 12.2; DB 3; Length 25;
Best Local Similarity 82.4%; Pred. No. 5.8e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 3 ATGGATGATACCGTCA 19
DB 6 ATGGGTGATACCGTCA 22
RESULT 30
US-08-614-686A-6
Sequence 6, Application US/08614686A
Patent No. 5830692
GENERAL INFORMATION:
APPLICANT: B CK, August; MYER, Dagmar; SCHLENSOG,
TITLE OF INVENTION: Express System Which Can Be
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Collard & Roe, P.C.
STREET: 1077 No. 5830692Ithern Boulevard
CITY: Roslyn
STATE: New York
COUNTRY: U.S.A.
ZIP: 11576
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordperfect Version 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/614,686A
FILING DATE: MARCH 12, 1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GR19510930
FILING DATE: 24 MARCH 1995
APPLICATION NUMBER: GR19514056.7
FILING DATE: 13 APRIL 1995
ATTORNEY/AGENT INFORMATION:
NAME: Collard, Allison C.
REGISTRATION NUMBER: 22,532
REFERENCE/DOCKET NUMBER: BOCK ET AL.-4
ATTORNEY/AGENT INFORMATION:
NAME: Freedman, Edward R.
REGISTRATION NUMBER: 26,048
REFERENCE/DOCKET NUMBER: BOCK ET AL.-4
ATTORNEY/AGENT INFORMATION:
NAME: Keusey, Edwin H.
REGISTRATION NUMBER: 34,361
REFERENCE/DOCKET NUMBER: BOCK ET AL.-4
TELECOMMUNICATION INFORMATION:

TELEPHONE: (516) 365-9802
TELEFAX: (516) 365-9805
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 29 base pairs
TYPE: nucleotide
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
IMMEDIATE SOURCE:
CLONE: PBUD200
POSITION IN GENOME:
UNITS: bp
US-08-614-686A-6
Query Match 61.0% Score 12.2; DB 2; Length 29;
Best Local Similarity 82.4%; Pred. No. 5.9e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 TTATGATGATACCGT 17
DB 13 TTATGAAAAGAAACCGT 29
Search completed: March 2, 2006, 01:01:34
Job time : 63.3333 secs

Db 1 TTATGGTTGATACGGT 17

RESULT 27

US-08-859-998-765
 ; Sequence 765, Application US/08859998
 ; Patent No. 594076
 ; GENERAL INFORMATION:
 ; APPLICANT: Chenchik, Alex
 ; APPLICANT: Johadze, George
 ; APPLICANT: Bibilashvili, Robert
 ; TITLE OF INVENTION: METHOD OF ASSAYING DIFFERENTIAL
 ; TITLE OF INVENTION: EXPRESSION
 ; NUMBER OF SEQUENCES: 1375
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Fish & Richardson, P.C.
 ; STREET: 2200 Sand Hill Road, Suite 100
 ; CITY: Menlo Park
 ; STATE: CA
 ; COUNTRY: US
 ; ZIP: 94025
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: Windows95
 ; SOFTWARE: FastSeq for Windows Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/859,998
 ; FILING DATE: 21-MAY-1997
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Field, Bret E.
 ; REGISTRATION NUMBER: 37,620
 ; REFERENCE/DOCKET NUMBER: 09096/002001
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 415-322-5070
 ; TELEFAX: 415-854-0875
 ; INFORMATION FOR SEQ ID NO: 765:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 25 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA
 ; FEATURE:
 ; OTHER INFORMATION: oligonucleotide primer
 ; US-08-859-998-765

Query Match 61.0%; Score 12.2; DB 2; Length 25;
 Best Local Similarity 82.4%; Pred. No. 5.8e+03;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 ATGAATGATACCGTCA 19
 |||||
 Db 6 ATGGGTGATACCGTCA 22

RESULT 28

US-09-225-928-765
 ; Sequence 765, Application US/09225928
 ; Patent No. 6352829
 ; GENERAL INFORMATION:
 ; APPLICANT: Chenchik, Alex
 ; APPLICANT: Johadze, George
 ; APPLICANT: Bibilashvili, Robert
 ; TITLE OF INVENTION: METHOD OF ASSAYING DIFFERENTIAL
 ; TITLE OF INVENTION: EXPRESSION
 ; NUMBER OF SEQUENCES: 1375
 ; CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson, P.C.
 STREET: 2200 Sand Hill Road, Suite 100
 CITY: Menlo Park
 STATE: CA
 COUNTRY: US
 ZIP: 94025

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: Windows95
 SOFTWARE: FastSeq for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/225,928
 FILING DATE: 05-Jan-1999
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/859,998
 FILING DATE: 21-MAY-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Field, Bret E.
 REGISTRATION NUMBER: 37,620
 REFERENCE/DOCKET NUMBER: 09096/002001
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-322-5070
 TELEFAX: 415-854-0875
 INFORMATION FOR SEQ ID NO: 765:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 25 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA
 FEATURE:
 OTHER INFORMATION: oligonucleotide primer
 ; US-09-225-928-765

Query Match 61.0%; Score 12.2; DB 3; Length 25;
 Best Local Similarity 82.4%; Pred. No. 5.8e+03;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 ATGAATGATACCGTCA 19
 |||||
 Db 6 ATGGGTGATACCGTCA 22

RESULT 29

US-09-225-201B-765
 ; Sequence 765, Application US/09225201B
 ; Patent No. 6489455
 ; GENERAL INFORMATION:
 ; APPLICANT: Chenchik, Alex
 ; APPLICANT: Johadze, George
 ; APPLICANT: Bibilashvili, Robert
 ; TITLE OF INVENTION: METHOD OF ASSAYING DIFFERENTIAL
 ; TITLE OF INVENTION: EXPRESSION
 ; NUMBER OF SEQUENCES: 1375
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Fish & Richardson, P.C.
 ; STREET: 2200 Sand Hill Road, Suite 100
 ; CITY: Menlo Park
 ; STATE: CA
 ; COUNTRY: US
 ; ZIP: 94025
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: Windows95
 ; SOFTWARE: FastSeq for Windows Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/225,201B
 ; FILING DATE: 05-Jan-1999
 ; CLASSIFICATION: <Unknown>

APPLICANT: Titz, Richard
TITLE OF INVENTION: RIBOZYME THERAPY FOR THE TREATMENT OF PROLIFERATIVE
TITLE OF INVENTION: SKIN AND EYE DISEASES
FILE REFERENCE: 480124.407
CURRENT APPLICATION NUMBER: US/09/696,791
CURRENT FILING DATE: 2000-10-25
NUMBER OF SEQ ID NOS: 4523
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 3914
LENGTH: 19
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: PCNA HH ribozyme binding site
US-09-696-791-3914

Query Match 61.0%; Score 12.2; DB 3; Length 19;
Best Local Similarity 82.4%; Pred. No. 5.6e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 TTGAAATGATACCGTCAT 20
DB 18 TGTAAATGATATCTTCAT 2

RESULT 24

US-09-526-193A-99
Sequence 99, Application US/09526193A
Patent No. 6617122
GENERAL INFORMATION:
APPLICANT: Hayden, Michael R.
APPLICANT: Brooks-Wilson, Angela R.
APPLICANT: Pimstone, Simon N.
TITLE OF INVENTION: METHODS AND REAGENTS FOR MODULATING
FILE REFERENCE: 50110/002005
CURRENT APPLICATION NUMBER: US/09/526,193A
CURRENT FILING DATE: 2000-03-15
PRIOR APPLICATION NUMBER: 60/124,702
PRIOR FILING DATE: 1999-03-15
PRIOR APPLICATION NUMBER: 60/138,048
PRIOR FILING DATE: 1999-06-08
PRIOR APPLICATION NUMBER: 60/139,600
PRIOR FILING DATE: 1999-06-17
PRIOR APPLICATION NUMBER: 60/151,977
PRIOR FILING DATE: 1999-09-01
NUMBER OF SEQ ID NOS: 287
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 99
LENGTH: 21
TYPE: DNA
ORGANISM: Homo sapiens
US-09-526-193A-99

Query Match 61.0%; Score 12.2; DB 3; Length 21;
Best Local Similarity 82.4%; Pred. No. 5.7e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TTATGAATGATACCGT 17
DB 1 TTACGGAATGATCCTGT 17

RESULT 25

US-09-916-510A-9
Sequence 9, Application US/09916510A
Patent No. 6544507
GENERAL INFORMATION:
APPLICANT: IGGO, RICHARD D.
APPLICANT: BRUNORI, MICHELE A.
TITLE OF INVENTION: ANTI-NEOPLASTIC VIRAL AGENTS
FILE REFERENCE: 604-596
CURRENT APPLICATION NUMBER: US/09/916,510A

CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: GB 9906815.7
PRIOR FILING DATE: 1999-03-24
NUMBER OF SEQ ID NOS: 48
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 9
LENGTH: 22
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-916-510A-9

Query Match 61.0%; Score 12.2; DB 3; Length 22;
Best Local Similarity 82.4%; Pred. No. 5.7e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 TTGAAATGATACCGTCAT 20
DB 1 TGCATTGTCACCGTCAT 17

RESULT 26

US-08-902-585-4
Sequence 4, Application US/08902585
Patent No. 5834276
GENERAL INFORMATION:
APPLICANT: Lawlor, Elizabeth
TITLE OF INVENTION: No. 5834276el Asparaginyl tRNA Synthetase
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/902,585
FILING DATE: 29-JUL-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/844,154
FILING DATE: 18-APR-1997
APPLICATION NUMBER: 9607993.4
FILING DATE: 18-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Gimm, Edward R.
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P31457-3/1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090
TELEX:
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
US-08-902-585-4

Query Match 61.0%; Score 12.2; DB 2; Length 24;
Best Local Similarity 82.4%; Pred. No. 5.8e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TTATGAATGATACCGT 17

```
; FEATURE:
; OTHER INFORMATION: Primer
US-09-488-265B-52

Query Match      63.0%; Score 12.6; DB 3; Length 31;
Best Local Similarity 78.9%; Pred. No. 3.7e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      1 TTATGGAATGATACCGTCA 19
        ||| ||| ||| ||| |||
Db      29 TTCTGGAATGATACCGTTA 11

RESULT 20
US-09-422-978-1307
; Sequence 1307, Application US/09422978
; Patent No. 6537751
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CG1
; CURRENT APPLICATION NUMBER: US/09/422,978
; EARLIER FILING DATE: 1999-10-20
; EARLIER APPLICATION NUMBER: US 09/298,850
; EARLIER FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 60/109,732
; EARLIER FILING DATE: 1998-11-23
; EARLIER APPLICATION NUMBER: US 60/082,614
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 1307
; LENGTH: 47
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: allele
; LOCATION: 24
; OTHER INFORMATION: 99-22712-242 : polymorphic base A or G
US-09-422-978-1307

Query Match      63.0%; Score 12.6; DB 3; Length 47;
Best Local Similarity 78.9%; Pred. No. 3.9e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      2 TATGGAATGATACCGTCAT 20
        ||| ||| ||| ||| |||
Db      1 TCTGTAATGATACGTTTCAT 19

RESULT 21
US-09-705-299-38/C
; Sequence 38, Application US/09705299
; Patent No. 6440737
; GENERAL INFORMATION:
; APPLICANT: Lex M. Cowseert
; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: ANTISENSE MODULATION OF CELLULAR APOPTOSIS SUSCEPTIBILITY GENE
; FILE REFERENCE: RTS-0174
; CURRENT APPLICATION NUMBER: US/09/705,299
; CURRENT FILING DATE: 2000-11-01
; NUMBER OF SEQ ID NOS: 86
; SEQ ID NO 38
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-705-299-38

Query Match      62.0%; Score 12.4; DB 3; Length 20;
Best Local Similarity 92.9%; Pred. No. 4.5e+03;
```

```
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      7 AATGATACCGTCAT 20
        ||| ||| ||| ||| |||
Db      14 AAAGATACCGTCAT 1

RESULT 22
US-08-288-663A-4
; Sequence 4, Application US/08288663A
; Patent No. 5878896
; GENERAL INFORMATION:
; APPLICANT: HINDMA, Shuji
; APPLICANT: HOSOYA, Masaki
; APPLICANT: ONDA, Haruo
; TITLE OF INVENTION: HUMAN TRH RECEPTOR, ITS PRODUCTION
; TITLE OF INVENTION: AND USE
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSMAN, LLP
; STREET: 130 Water Street
; City: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/288,663A
; FILING DATE: 09-AUG-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 198309/1993
; FILING DATE: 10-AUG-1993
; APPLICATION NUMBER: 286986/1993
; FILING DATE: 16-NOV-1993
; APPLICATION NUMBER: 325215/1993
; FILING DATE: 22-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Resnick, David S
; REGISTRATION NUMBER: 34,235
; REFERENCE/DOCKET NUMBER: 44612
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-523-3400
; TELEFAX: 617-523-6440
; TELEX:
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 37 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Other nucleic acid, synthetic DNA
US-08-288-663A-4

Query Match      62.0%; Score 12.4; DB 2; Length 37;
Best Local Similarity 92.9%; Pred. No. 4.8e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      6 GAATGATACCGTCA 19
        ||| ||| ||| ||| |||
Db      20 GAATGAATACCGTCA 33

RESULT 23
US-09-696-791-3914/C
; Sequence 3914, Application US/09696791
; Patent No. 6770633
; GENERAL INFORMATION:
; APPLICANT: Robbins, Joan M.
```

```
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: DK 0420/92
;; FILING DATE: 27-MAR-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: DK PCT/DK93/00109
;; FILING DATE: 29-MAR-1993
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Lowney Dr., Karen A.
;; REGISTRATION NUMBER: 31,274
;; REFERENCE/DOCKET NUMBER: 3730.204-US
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 212-867-0123
;; TELEFAX: 212-878-9655
;; INFORMATION FOR SEQ ID NO: 5:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 60 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: cDNA
;; US-08-313-050-5

Query Match      64.0%; Score 12.8; DB 2; Length 60;
Best Local Similarity 87.5%; Pred. No. 3.1e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      4 TGAATGATACCGTCA 19
        |||||
Db      21 TGAATGCCACCGTCA 36

RESULT 16
US-09-396-196G-10050/c
; Sequence 10050, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Miltmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396.196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq For Windows Version 4.0
; SEQ ID NO 10050
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-10050

Query Match      63.0%; Score 12.6; DB 3; Length 25;
Best Local Similarity 78.9%; Pred. No. 3.6e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      1 TTATGATGATACCGTCA 19
        |||||
Db      19 TTATGAAGAAGATGCCCTTA 1

RESULT 17
US-09-684-855-28/c
; Sequence 28, Application US/09684855
; Patent No. 659735
; GENERAL INFORMATION:
; APPLICANT: F. Hoffmann-La Roche AG
; TITLE OF INVENTION: CONTINUOUS FERMENTATION PROCESS
; FILE REFERENCE: C38435/111692
; CURRENT APPLICATION NUMBER: US/09/684.855
; CURRENT FILING DATE: 2000-10-06
```

```
;; PRIOR APPLICATION NUMBER: EP 00121663.9
;; PRIOR FILING DATE: 2000-10-04
;; PRIOR APPLICATION NUMBER: EP 99120289.6
;; PRIOR FILING DATE: 1999-10-11
;; NUMBER OF SEQ ID NOS: 169
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 28
;; LENGTH: 31
;; TYPE: DNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence:Primer
US-09-684-855-28

Query Match      63.0%; Score 12.6; DB 3; Length 31;
Best Local Similarity 78.9%; Pred. No. 3.7e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      1 TTATGATGATACCGTCA 19
        |||||
Db      29 TTCTGATATATACCGTTA 11

RESULT 18
US-09-684-855-29
; Sequence 29, Application US/09684855
; Patent No. 659735
; GENERAL INFORMATION:
; APPLICANT: F. Hoffmann-La Roche AG
; TITLE OF INVENTION: CONTINUOUS FERMENTATION PROCESS
; FILE REFERENCE: C38435/111692
; CURRENT APPLICATION NUMBER: US/09/684.855
; CURRENT FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: EP 00121663.9
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: EP 99120289.6
; PRIOR FILING DATE: 1999-10-11
; NUMBER OF SEQ ID NOS: 169
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 29
; LENGTH: 31
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Primer
US-09-684-855-29

Query Match      63.0%; Score 12.6; DB 3; Length 31;
Best Local Similarity 78.9%; Pred. No. 3.7e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      1 TTATGATGATACCGTCA 19
        |||||
Db      3 TTCTGATATATACCGTTA 21

RESULT 19
US-09-488-265B-52/c
; Sequence 52, Application US/09488265B
; Patent No. 6720174
; GENERAL INFORMATION:
; APPLICANT: Lehmann, Martin
; APPLICANT: Lassen, Soren F
; TITLE OF INVENTION: Improved Phytases
; FILE REFERENCE: 5808.200-US
; CURRENT APPLICATION NUMBER: US/09/488.265B
; CURRENT FILING DATE: 2000-01-20
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 52
; LENGTH: 31
; TYPE: DNA
; ORGANISM: Artificial Sequence
```

```

; SEQ ID NO 18886
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-18886

```

Query Match	66.0%;	Score 13.2;	DB 3;	Length 25;
Best Local Similarity	83.3%;	Pred. No. 1.8e+03;		
Matches 15; Conservative	0;	Mismatches 3;	Indels 0;	Gaps 0;

```

QY      2 TATGGAATGATACCGTCA 19
          |||||
Db     18 TATGGAATGACCAAGGTCA 1

```

RESULT 12
US-10-131-827-3115
; Sequence 3115, Application US/10131827
; Patent No. 6905927

: APPLICANT: Wohlgemuth, Jay
 : APPLICANT: Fry, Kirk
 : APPLICANT: Woodward, Robert
 : APPLICANT: Ly, Ngoc
 : TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE
 : TITLE OF INVENTION: CHRONIC INFLAMMATORY DISEASES
 : TITLE OF INVENTION:

```

CURRENT FILING DATE:    2002-09-06
PRIORITY APPLICATION NUMBER: US 10/006,290
PRIOR FILING DATE:      2001-10-22
PRIORITY APPLICATION NUMBER: US 60/296,764
PRIOR FILING DATE:      2001-06-08
NUMBER OF SEQ ID NOS:   9090
SOFTWARE: PatentIn version 3.1
SEQ ID NO 3115
LENGTH: 50
TYPE: DNA
ORGANISM: Homo sapiens
US-10-131-827-3115
```

Query Match	66.0%;	Score 13.2;	DB 3;	Length 50;
Best Local Similarity	83.3%;	Pred. No. 1.9e+03;		
Matches 15; Conservative	0;	Mismatches 3;	Indels 0;	Gaps 0

```

Qy      2 TATGGAATGATACCGTCA 19
          |||||
Db      13 TTTGGAATGATACCCACA 30

```

RESULT 13
US-10-131-827-7377
; Sequence 7377, Application US/10131827
; Patent No. 5005007

APPLICANT: Wohlgenuth, Jay
 APPLICANT: Fry, Kirk
 APPLICANT: Woodward, Robert
 APPLICANT: Ly, Ngoc
 TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE
 TITLE OF INVENTION: CHRONIC INFLAMMATORY DISEASES

```

? CURRENT APPLICATION NUMBER: US/10/131,827
?
? CURRENT FILING DATE: 2002-09-06
?
? PRIOR APPLICATION NUMBER: US 10/006,290
?
? PRIOR FILING DATE: 2001-10-22
?
? PRIOR APPLICATION NUMBER: US 60/296,764
?
? PRIOR FILING DATE: 2001-06-08
?
? NUMBER OF SEQ ID NOS: 9090
?
? SOFTWARE: PatentIn version 3.1
?
? SEQ ID NO 7377
?
? LENGTH: 50
?
? TYPE: DNA

```

ORGANISM: Homo sapiens
US-10-131-827-7377

Query Match	66.0%	Score 13.2;	DB 3;	length 50;
Best Local Similarity	83.3%	Pred. No. 1.9e+03;		
Matches 15; Conservative	0;	Mismatches 3;	Indels 0;	Gaps 0;

Qy	2	TATGAATGATACCGTCA	19
Db	7	TATGAATGAGACCACCA	24

RESULT 14
US-09-396-196G-75543

Patent No. 6821724
GENERAL INFORMATION:
APPLICANT: Michael Mittmann

```

? APPLICANT: Affymetrix, Inc.
? TITLE OF INVENTION: Methods of Genetic Analysis
? FILE REFERENCE: 3101.1
? CURRENT APPLICATION NUMBER: US/09/396,196G
? CURRENT FILING DATE: 1999-09-15
? PRIOR APPLICATION NUMBER: 60/100,678
? PRIOR FILING DATE: 1998-09-17
? NUMBER OF SEQ ID NOS: 127806
? SOFTWARE: PasteSeq for Windows Version 4.0
? SEQ ID NO: 75543
? LENGTH: 25
? TYPE: DNA
? ORGANISM: mus musculus
US-09-396-196G-75543

```

Query Match	64.0%;	Score 12.8;	DB 3;	Length 25;
Best Local Similarity	87.5%;	Pred. No. 2.8e+03;		
Matches 14; Conservative	0;	Mismatches 2;	Indels 0;	Gaps 0;

```
Qy      2 TATGGAATGATACCGT 17
         ||||| | |||||
Db      2 TATGGAACGCTACCGT 17
```

RESULT 15
US-08-313-050-5
; Sequence 5, Application US/08313050
; Patent No. 5585256

? APPLICANT: Dorreich, Kurt
 ? APPLICANT: Christensen, Flemming M.
 ? APPLICANT: Schnell, Yvette
 ? APPLICANT: Mischler, Marcel
 ? APPLICANT: Dalbog, Henrik
 ? APPLICANT: Heildt-Hansen, Hans P.
 ? TITLE OF INVENTION: A NOVEL ENZYME AND A DNA SEQUENCE
 ? NUMBER OF SEQUENCES: 18

ADDRESS: 405 Lexington Avenue, 64th Floor
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/313,050
FILING DATE: 05-OCT-1994
CLASSIFICATION: 435


```
FILE REFERENCE: HIRAI150
CURRENT APPLICATION NUMBER: US/09/463,702A
CURRENT FILING DATE: 2000-01-24
PRIORITY APPLICATION NUMBER: PCT/JP98/03114
PRIOR FILING DATE: 1998-07-10
PRIOR APPLICATION NUMBER: JAPAN 9/200387
PRIOR FILING DATE: 1997-07-25
NUMBER OF SEQ ID NOS: 44
SOFTWARE: Patentin version 3.0
SEQ ID NO 25
LENGTH: 24
TYPE: DNA
ORGANISM: ARTIFICIAL
FEATURE:
OTHER INFORMATION: PRIMER 3' GSP2
US-09-463-702A-25
```

```
Query Match      66.0%; Score 13.2; DB 3; Length 24;
Best Local Similarity 83.3%; Pred. No. 1.7e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
Oy      1 TTATGATGATACCGTC 18
         |||||
Db      5 TCATGATGATCCTGTC 22
```

```
RESULT 8
US-09-699-135-25
Sequence 25, Application US/09699135
Patent No. 6472513
GENERAL INFORMATION:
APPLICANT: AGENE Research Institute, Co., Ltd.
APPLICANT: HIRAKI AND ASSOCIATES
APPLICANT: SHIMAMOTO, AKIRO
APPLICANT: KITAO, SAORI
APPLICANT: FURUICHI, YASUHIRO
TITLE OF INVENTION: HUMAN GENE RECO4 ENCODING HELICASE
FILE REFERENCE: HIRAI150
CURRENT APPLICATION NUMBER: US/09/699,135
CURRENT FILING DATE: 2000-10-27
PRIOR APPLICATION NUMBER: US/09/463,702A
PRIOR FILING DATE: 2000-01-24
PRIOR APPLICATION NUMBER: PCT/JP98/03114
PRIOR FILING DATE: 1998-07-10
PRIOR APPLICATION NUMBER: JAPAN 9/200387
PRIOR FILING DATE: 1997-07-25
NUMBER OF SEQ ID NOS: 44
SOFTWARE: Patentin version 3.0
SEQ ID NO 25
LENGTH: 24
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: PRIMER 3' GSP2
US-09-699-135-25
```

```
Query Match      66.0%; Score 13.2; DB 3; Length 24;
Best Local Similarity 83.3%; Pred. No. 1.7e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
Oy      1 TTATGATGATACCGTC 18
         |||||
Db      5 TCATGATGATCCTGTC 22
```

```
RESULT 9
US-09-396-196G-15329/c
Sequence 15329, Application US/09396196G
Patent No. 6821724
GENERAL INFORMATION:
APPLICANT: Michael Miltmann
APPLICANT: David Mack
APPLICANT: David Lockhart
```

```
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
CURRENT APPLICATION NUMBER: US/09/396,196G
CURRENT FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: 60/100,678
PRIOR FILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 15329
LENGTH: 25
TYPE: DNA
ORGANISM: Mus musculus
US-09-396-196G-15329
```

```
Query Match      66.0%; Score 13.2; DB 3; Length 25;
Best Local Similarity 83.3%; Pred. No. 1.8e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
Oy      3 ATGATGATACCGTCAT 20
         |||||
Db      24 ATAGACTGATACGTCAT 7
```

```
RESULT 10
US-09-396-196G-18885/c
Sequence 18885, Application US/09396196G
Patent No. 6821724
GENERAL INFORMATION:
APPLICANT: Michael Miltmann
APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
CURRENT APPLICATION NUMBER: US/09/396,196G
CURRENT FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: 60/100,678
PRIOR FILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 18885
LENGTH: 25
TYPE: DNA
ORGANISM: Mus musculus
US-09-396-196G-18885
```

```
Query Match      66.0%; Score 13.2; DB 3; Length 25;
Best Local Similarity 83.3%; Pred. No. 1.8e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
Oy      2 TATGATGATACCGTCA 19
         |||||
Db      21 TATGATGATACGTCAT 4
```

```
RESULT 11
US-09-396-196G-18886/c
Sequence 18886, Application US/09396196G
Patent No. 6821724
GENERAL INFORMATION:
APPLICANT: Michael Miltmann
APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
CURRENT APPLICATION NUMBER: US/09/396,196G
CURRENT FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: 60/100,678
PRIOR FILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FastSeq for Windows Version 4.0
```

```

; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/592,936
; FILING DATE: 29-JAN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Evans, Susan T.
; REGISTRATION NUMBER: 38,443
; REFERENCE/DOCKET NUMBER: 4257-0012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 324-0880
; TELEFAX: (650) 324-0960
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: Drugen 3' primer
; US-09-111-573-7

```

```

Query Match      71.0%; Score 14.2; DB 2; Length 22;
Best Local Similarity 84.2%; Pred. No. 5.3e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```

```

QY      1 TTATGATGATGATCGCTCA 19
Db      20 TTATGCACTATATACCGTCA 2

```

```

RESULT 4
US-09-959-650-16/C
; Sequence 16, Application US/09959650
; Patent No. 6919198
; GENERAL INFORMATION:
; APPLICANT: timo Korpela et al.
; TITLE OF INVENTION: Microbial protein expression system
; FILE REFERENCE: 0933-0175P
; CURRENT APPLICATION NUMBER: US/09/959,650
; CURRENT FILING DATE: 2002-02-26
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleotide primer
US-09-959-650-16

```

```

Query Match      71.0%; Score 14.2; DB 3; Length 26;
Best Local Similarity 84.2%; Pred. No. 5.4e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```

```

QY      1 TTATGATGATGATCGCTCA 19
Db      21 TTACGGATGATGATCGACA 3

```

```

RESULT 5
US-09-422-978-1662
; Sequence 1662, Application US/09422978
; Patent No. 6537751
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marca
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CP1
; CURRENT APPLICATION NUMBER: US/09/422,978

```

```

; CURRENT FILING DATE: 1999-10-20
; EARLIER APPLICATION NUMBER: US 09/298,850
; EARLIER FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 60/109,732
; EARLIER FILING DATE: 1998-11-23
; EARLIER APPLICATION NUMBER: US 60/082,614
; EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 1662
; LENGTH: 47
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: allele
; LOCATION: 24
; OTHER INFORMATION: 99-5447-322 : polymorphic base A or G
; US-09-422-978-1662

```

```

Query Match      68.0%; Score 13.6; DB 3; Length 47;
Best Local Similarity 80.0%; Pred. No. 1.2e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```

```

QY      1 TTATGATGATGATCGCTCAT 20
Db      27 TTATATAAAGATTCGCTCAT 46

```

```

RESULT 6
US-10-131-827-3668
; Sequence 3668, Application US/10131827
; Patent No. 6905827
; GENERAL INFORMATION:
; APPLICANT: Wohlgenuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMM
; FILE REFERENCE: 506612000120
; CURRENT APPLICATION NUMBER: US/10/131,827
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: US 10/006,290
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/296,764
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 9090
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3668
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-131-827-3668

```

```

Query Match      68.0%; Score 13.6; DB 3; Length 50;
Best Local Similarity 80.0%; Pred. No. 1.2e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```

```

QY      1 TTATGATGATGATCGCTCAT 20
Db      17 TTGTGGAATGATGATCTAAT 36

```

```

RESULT 7
US-09-463-702A-25
; Sequence 25, Application US/09463702A
; Patent No. 6335435
; GENERAL INFORMATION:
; APPLICANT: AGENE Research Institute, Co., Ltd.
; APPLICANT: HIRAKI AND ASSOCIATES
; APPLICANT: SHIMOTO, AKIRO
; APPLICANT: KITAO, SAORI
; APPLICANT: FURUICHI, YASUHIRO
; TITLE OF INVENTION: HUMAN GENE RECO4 ENCODING HELICASE

```

C 98 11.6 58.0 27 3 US-08-469-419-36 Sequence 36, Appl
C 99 11.6 58.0 27 3 US-08-469-419-38 Sequence 38, Appl
C 100 11.6 58.0 31 3 US-08-934-386-42 Sequence 42, Appl

ALIGNMENTS

RESULT 1

US-08-592-936B-7/c
; Sequence 7, Application US/08592936B
; Patent No. 5783393
; GENERAL INFORMATION:
; APPLICANT: Kelllogg, Jill A.
; APPLICANT: Bestwick, Richard K.
; TITLE OF INVENTION: PLANT TISSUE / STAGE SPECIFIC PROMOTERS FOR
; TITLE OF INVENTION: REGULATED EXPRESSION OF TRANSGENES IN PLANTS
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Avenue, Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/592,936B
; FILING DATE: 29-JAN-1996
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Evans, Susan T.
; REGISTRATION NUMBER: 38,443
; REFERENCE/DOCKET NUMBER: 4257-0012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 324-0880
; TELEFAX: (650) 324-0960
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: Drugen 3' primer
US-08-592-936B-7

Query Match 71.0%; Score 14.2; DB 2; Length 22;
Best Local Similarity 84.2%; Pred. No. 5.3e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

CY 1 TTATGATGATACCGTCA 19
DB 20 TTATGACTATACCGTCA 2

RESULT 2

US-08-788-928A-18/c
; Sequence 18, Application US/08788928A
; Patent No. 5783394
; GENERAL INFORMATION:
; APPLICANT: Bestwick, Richard K.
; APPLICANT: Kelllogg, Jill A.
; TITLE OF INVENTION: RASPBERRY PROMOTERS FOR EXPRESSION OF
; TITLE OF INVENTION: TRANSGENES IN PLANTS
; NUMBER OF SEQUENCES: 25

CORRESPONDENCE ADDRESS:

ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/788,928A

FILING DATE: 24-JAN-1997

CLASSIFICATION: 800

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/592,936

FILING DATE: 29-JAN-1996

ATTORNEY/AGENT INFORMATION:
NAME: Evans, Susan T.

REGISTRATION NUMBER: 38,443

REFERENCE/DOCKET NUMBER: 4257-0015

TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 324-0880

TELEFAX: (650) 324-0960

INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:

LENGTH: 22 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Drugen 3' primer

US-08-788-928A-18

Query Match 71.0%; Score 14.2; DB 2; Length 22;
Best Local Similarity 84.2%; Pred. No. 5.3e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

CY 1 TTATGATGATACCGTCA 19
DB 20 TTATGACTATACCGTCA 2

RESULT 3

US-09-111-573-7/c
; Sequence 7, Application US/09111573
; Patent No. 5929302
; GENERAL INFORMATION:
; APPLICANT: Kelllogg, Jill A.
; APPLICANT: Bestwick, Richard K.
; TITLE OF INVENTION: PLANT TISSUE / STAGE SPECIFIC PROMOTERS FOR
; TITLE OF INVENTION: REGULATED EXPRESSION OF TRANSGENES IN PLANTS
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Avenue, Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/111,573
; FILING DATE:

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: March 2, 2006, 00:58:14 ; Search time 62.3333 Seconds
(without alignments)
570.341 Million cell updates/sec

Title: US-10-653-528-33
Perfect score: 20
Sequence: 1 ttatggaatgataccgctcat 20

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues
Total number of hits satisfying chosen parameters: 1395746

Minimum DB seq length: 0
Maximum DB seq length: 80

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : Issued_Patente.NA.*
1: /cgn2_6/ptodata/1/ina/1_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/H_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/PTCUS_COMB.seq:*
7: /cgn2_6/ptodata/1/ina/PP_COMB.seq:*
8: /cgn2_6/ptodata/1/ina/RE_COMB.seq:*
9: /cgn2_6/ptodata/1/ina/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	14.2	71.0	22	2	US-08-592-9368-7 Sequence 7, Appl1
2	14.2	71.0	22	2	US-08-788-928A-18 Sequence 18, Appl1
3	14.2	71.0	22	2	US-09-111-573-7 Sequence 7, Appl1
4	14.2	71.0	26	3	US-09-959-650-16 Sequence 16, Appl1
5	13.6	68.0	47	3	US-09-422-978-1662 Sequence 1662, Ap
6	13.6	68.0	50	3	US-10-131-827-3668 Sequence 3668, Ap
7	13.2	66.0	24	3	US-09-463-702A-25 Sequence 25, Appl1
8	13.2	66.0	24	3	US-09-699-135-25 Sequence 25, Appl1
9	13.2	66.0	25	3	US-09-396-196G-15329 Sequence 15329, A
10	13.2	66.0	25	3	US-09-396-196G-18885 Sequence 18885, A
11	13.2	66.0	25	3	US-09-396-196G-18886 Sequence 18886, A
12	13.2	66.0	50	3	US-10-131-827-3115 Sequence 3115, Ap
13	13.2	66.0	50	3	US-10-131-827-7377 Sequence 7377, Ap
14	12.8	64.0	25	3	US-09-396-196G-75543 Sequence 75543, A
15	12.8	64.0	60	2	US-08-313-050-5 Sequence 5, Appl1
16	12.6	63.0	25	3	US-09-396-196G-10050 Sequence 10050, A
17	12.6	63.0	31	3	US-09-684-855-28 Sequence 28, Appl1
18	12.6	63.0	31	3	US-09-684-855-29 Sequence 29, Appl1
19	12.6	63.0	31	3	US-09-488-265B-52 Sequence 52, Appl1
20	12.6	62.0	47	3	US-09-422-978-1307 Sequence 1307, Ap
21	12.4	62.0	20	3	US-09-705-299-38 Sequence 38, Appl1
22	12.4	62.0	37	2	US-08-288-663A-4 Sequence 4, Appl1
23	12.2	61.0	19	3	US-09-696-791-3914 Sequence 3914, Ap
24	12.2	61.0	21	3	US-09-526-193A-99 Sequence 99, Appl1

25	12.2	61.0	22	3	US-09-916-510A-9 Sequence 9, Appl1
26	12.2	61.0	24	2	US-08-902-585-4 Sequence 4, Appl1
27	12.2	61.0	25	2	US-08-859-998-765 Sequence 765, App
28	12.2	61.0	25	3	US-09-225-928-765 Sequence 765, App
29	12.2	61.0	25	3	US-09-225-928B-765 Sequence 6, Appl1
30	12.2	61.0	29	2	US-08-614-686A-6 Sequence 15, Appl1
31	12.2	61.0	36	2	US-08-614-686A-15 Patent No. 5318899
32	12.2	61.0	37	9	5318899-32
33	12.2	61.0	70	3	US-08-961-888-14 Sequence 14, Appl1
34	12	60.0	25	3	US-09-217-101-5 Sequence 5, Appl1
35	12	60.0	25	3	US-09-396-196G-40480 Sequence 40480, A
36	12	60.0	25	3	US-09-396-196G-90391 Sequence 90391, A
37	12	60.0	25	3	US-09-396-196G-90747 Sequence 90747, A
38	12	60.0	32	3	US-09-396-196G-120208 Sequence 120208,
39	12	60.0	32	3	US-09-091-348-4 Sequence 4, Appl1
40	12	60.0	39	2	US-08-678-369-10 Sequence 10, Appl1
41	12	60.0	39	2	US-09-047-243-10 Sequence 10, Appl1
42	12	60.0	42	2	US-08-381-666-2 Sequence 2, Appl1
43	12	60.0	42	2	US-08-381-370-2 Sequence 2, Appl1
44	12	60.0	42	2	US-08-381-034-2 Sequence 2, Appl1
45	12	60.0	42	2	US-08-381-040-3 Sequence 2, Appl1
46	12	60.0	42	2	US-08-384-183-3 Sequence 3, Appl1
47	12	60.0	42	2	US-08-384-292-3 Sequence 3, Appl1
48	12	60.0	42	2	US-08-383-631-3 Sequence 3, Appl1
49	12	60.0	42	2	US-08-383-639-3 Sequence 3, Appl1
50	12	60.0	42	2	US-08-381-037-2 Sequence 2, Appl1
51	12	60.0	42	2	US-08-381-050-2 Sequence 2, Appl1
52	12	60.0	42	2	US-08-381-163-2 Sequence 2, Appl1
53	12	60.0	42	2	US-08-381-041A-2 Sequence 2, Appl1
54	12	60.0	42	2	US-08-383-649-2 Sequence 2, Appl1
55	12	60.0	42	2	US-08-381-054-2 Sequence 2, Appl1
56	12	60.0	42	2	US-08-383-632-2 Sequence 2, Appl1
57	12	60.0	42	2	US-08-381-059-2 Sequence 2, Appl1
58	12	60.0	42	2	US-08-381-047-2 Sequence 4, Appl1
59	12	60.0	42	2	US-08-384-492-2 Sequence 2, Appl1
60	12	60.0	42	2	US-08-442-916-2 Sequence 2, Appl1
61	12	60.0	42	2	US-08-429-362-4 Sequence 4, Appl1
62	12	60.0	42	2	US-08-383-650-2 Sequence 2, Appl1
63	12	60.0	42	2	US-08-678-369-9 Sequence 9, Appl1
64	12	60.0	42	2	US-08-905-694-2 Sequence 2, Appl1
65	12	60.0	42	2	US-09-047-243-9 Sequence 9, Appl1
66	12	60.0	42	2	US-09-313-221A-105 Sequence 105, App
67	12	60.0	66	2	US-08-788-943A-16 Sequence 16, Appl1
68	12	60.0	66	2	US-09-176-664-23 Sequence 23, Appl1
69	11.8	59.0	24	3	US-09-519-076-23 Sequence 5, Appl1
70	11.8	59.0	29	3	US-08-614-686A-5 Sequence 5, Appl1
71	11.8	59.0	29	3	US-09-304-232-481 Sequence 481, App
72	11.8	59.0	33	3	US-09-486-356-15 Sequence 15, Appl1
73	11.8	59.0	33	3	US-09-577-528B-15 Sequence 15, Appl1
74	11.8	59.0	33	3	US-10-208-557-15 Sequence 15, Appl1
75	11.8	59.0	35	3	US-09-581-941-4 Sequence 4, Appl1
76	11.8	59.0	35	3	US-09-084-303B-73 Sequence 73, Appl1
77	11.8	59.0	40	2	US-08-614-686A-13 Sequence 5, Appl1
78	11.8	59.0	41	3	US-10-225-323A-5 Sequence 5, Appl1
79	11.8	59.0	41	3	US-10-225-323A-6 Sequence 6, Appl1
80	11.8	59.0	56	2	US-08-621-976A-16260 Sequence 2, Appl1
81	11.8	59.0	56	3	US-09-621-976A-16260 Sequence 16260, A
82	11.8	59.0	59	3	US-09-573-080A-49 Sequence 49, Appl1
83	11.8	59.0	59	3	US-08-526-840B-109 Sequence 109, App
84	11.6	58.0	20	2	US-08-624-545-48 Sequence 48, Appl1
85	11.6	58.0	20	2	US-08-624-545-48 Sequence 49, Appl1
86	11.6	58.0	24	2	US-08-066-325-49 Sequence 5, Appl1
87	11.6	58.0	24	3	US-09-440-005-5 Sequence 5, Appl1
88	11.6	58.0	25	2	US-08-743-637B-109 Sequence 109, App
89	11.6	58.0	25	3	US-08-526-840B-109 Sequence 109, App
90	11.6	58.0	25	3	US-09-396-196G-90748 Sequence 90748, A
91	11.6	58.0	25	3	US-09-396-196G-100746 Sequence 100746,
92	11.6	58.0	27	2	US-08-411-795B-36 Sequence 36, Appl1
93	11.6	58.0	27	2	US-08-411-795B-38 Sequence 38, Appl1
94	11.6	58.0	27	2	US-08-469-318A-36 Sequence 36, Appl1
95	11.6	58.0	27	2	US-08-469-318A-38 Sequence 38, Appl1
96	11.6	58.0	27	3	US-08-764-114-36 Sequence 36, Appl1
97	11.6	58.0	27	3	US-08-764-114-38 Sequence 38, Appl1

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RESULT 29
BH911786/c 41 bp DNA linear GSS 04-SEP-2002
LOCUS SALK_072158.26.45.x Arabidopsis thaliana T-DNA insertion lines
DEFINITION Arabidopsis thaliana genomic clone SALK_072158.26.45.x, genomic survey sequence.

ACCESSION BH911786
VERSION BH911786.1 GI:22724719
KEYWORDS GSS.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana

REFERENCE
AUTHORS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 41)
Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R., Gadgil, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L., Shinn, P., Zimmermann, J., and Ecker, J.R.
A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome
Unpublished (2001)
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of T-DNA.
Class: T-DNA tagged.
Location/Qualifiers
1..41
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/ecotype="Col-0"
/db_xref="taxon:3702"
/clone="SALK_072158.26.45.x"
/note="PCR was performed on Arabidopsis thaliana T-DNA insertion lines" each of which contains one or more T-DNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"

ORIGIN

Query Match 61.0%; Score 12.2; DB 9; Length 41;
Best Local Similarity 82.4%; Pred. No. 1.4e+05;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TATGGAATGATACCGTC 18
|||||
DB 23 TATGGAATGATACCGTC 7

RESULT 30
AL952980 42 bp DNA linear GSS 02-APR-2004
LOCUS Arabidopsis thaliana T-DNA flanking sequence GK-347E08-016235,
DEFINITION genomic survey sequence.
ACCESSION AL952980
VERSION AL952980.1 GI:24409602
KEYWORDS GSS.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana

REFERENCE
AUTHORS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1
Li, Y., Rosso, M.G., Strizhov, N., Viehoveer, P., and Weishaar, B.
GABI-Kat SimpleSearch: a flanking sequence tag (FST) database for

the identification of T-DNA insertion mutants in Arabidopsis thaliana
Bioinformatics 19 (11), 1441-1442 (2003)
12874060

REFERENCE
AUTHORS Rosso, M.G., Li, Y., Strizhov, N., Reiss, B., Dekker, K. and Weishaar, B.
An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for flanking sequence tag-based reverse genetics
Plant Mol. Biol. 53 (1-2), 247-259 (2003)
14756321

REFERENCE
AUTHORS Strizhov, N., Li, Y., Rosso, M.G., Viehoveer, P., Dekker, K.A. and Weishaar, B.
High-throughput generation of sequence indexes from T-DNA mutagenized Arabidopsis thaliana lines
Biotechniques 35 (6), 1164-1168 (2003)
14682050

JOURNAL
PUBMED 4 (bases 1 to 42)
Rosso, M.G., Li, Y., Strizhov, N. and Weishaar, B.
Direct Submission
Submitted (31-MAR-2004) Weishaar B., Max-Planck-Institut fuer Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
This sequence has been recovered from the left border of the T-DNA. It indicates an insertion within the locus defined by BAC clone MVA11. Details on the protocols used for generation of the sequence are described in References 1-3. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat project. GABI-Kat is part of the German Plant Genomics program designated 'GABI'. Information on line availability can be found at: <http://www.mpiz-koeln.mpg.de/GABI-Kat/>.
Location/Qualifiers
1..42
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/db_xref="taxon:3702"
/clone="GK-347E08-016235"
/clone_1lb="Arabidopsis thaliana T-DNA insertion lines"
/ecotype="Col-0"
/note="PCR was performed on DNA from Arabidopsis thaliana plants (T1) which were transformed with the T-DNA from vector pNC161 (Genbank accession number: AF537514). The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed."

ORIGIN

Query Match 61.0%; Score 12.2; DB 10; Length 42;
Best Local Similarity 82.4%; Pred. No. 1.4e+05;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 ATGGAATGATACCGTCA 19
|||||
DB 15 ATGGAATGATACCGCCA 31

Search completed: March 2, 2006, 01:14:32
Job time : 2945 secs

/organism="Sorghum bicolor"
/mol_type="genomic DNA"
/cultivar="BTx623"
/db_xref="taxon:4558"
/issue_type="leaves"
/dev_stage="seedling"
/clone_lib="Sorghum bicolor SUCot"
/note="Vector: pGBM-TA-Rasy; A Cot analysis was performed for the sorghum genome. Based on the resulting Cot curve, hydroxyapatite chromatography was used to isolate 'highly-repetitive' (HR), 'moderately-repetitive' (MR), and 'single/low-copy' (SL) sequence components from sheared genomic DNA. The three repetition-based DNA components were cloned into E. coli to produce HRCot, MRcot, and SLCot genomic libraries. Blotting and sequencing data indicates that each library is representative of the component from which it was derived. Putative ID listings given for sequences are based on comparison (blastn) with sequences in the NCBI Nr database. Only the primary match is given (all primary E values are < or = 1.00E-5). In no instance does a 'Cot clone' contain the complete sequence of its putative Nr match."

ORIGIN

Query Match 62.0%; Score 12.4; DB 9; Length 72;
Best Local Similarity 92.9%; Pred. No. 1.1e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 TGGATGATACCGT 17
|||
63 TGAATGATACCGT 50

RESULT 27
LOCUS CM233625 78 bp DNA linear GSS 30-OCT-2004
DEFINITION 104 687_11213545_116 37381_015 Sorghum methylation filtered library (LibID: 104) Sorghum bicolor genomic clone 11213545, genomic survey sequence.
ACCESSION CM233625
VERSION CM233625.1 GI:54942452
KEYWORDS GSS.
SOURCE Sorghum bicolor (sorghum)
ORGANISM Sorghum bicolor
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Sorghum.
1 (bases 1 to 78)
Bedell,J.A., Budiman,M.A., Nunberg,A., Citek,R.W., Robbins,D., Jones,J., Flick,E., Rohlfing,T., Fries,J., Bradford,K., McMenamy,J., Smith,M., Holman,H., Roe,B.A., Wiley,G., Korff,I.F., Rabinowicz,P.D., Lakey,N., McComble,W.R., Jeddeloh,J.A. and Martienssen,R.A.
Sorghum genome sequencing by methylation filtration
PLOS Biol. 3 (1), e13 (2005)
15660154
Contact: Bedell JJC
Orion Genomics, LLC
4041 Forest Park Ave, St. Louis, MO 63108, USA
Tel: 314 615 6979
Fax: 314 615 5975
Email: jbedell@oriongenomics.com
Plate: 687 row: b column: 01
Seq primer: T3 Reverse
Class: methylation filtered
High quality sequence stop: 78.
Location/Qualifiers
1..78
/organism="Sorghum bicolor"
/mol_type="genomic DNA"
/cultivar="BTx623"
/db_xref="taxon:4558"

FEATURES
source

/clone="11213545"
/clone_lib="Sorghum methylation filtered library (LibID: 104)"
/note="Organ: leaf; Vector: pBCK(-); Site 1: HindII; DNA prepared from purified nuclei was randomly sheared, end-repaired, size fractionated to enrich for the 0.5 to 5 kb fraction, ligated into HindII-digested pBCK(-) vector and electroporated into E. coli cells. This is a methylation filtered library."

ORIGIN

Query Match 62.0%; Score 12.4; DB 10; Length 78;
Best Local Similarity 92.9%; Pred. No. 1.2e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 TGGATGATACCGT 17
|||
55 TGAATGATACCGT 68

RESULT 28
LOCUS CL528379/c 80 bp DNA linear GSS 17-MAY-2004
DEFINITION ASV12806.fwd ASLV-vector integration sites in human 293T-TVA cells
Homo sapiens genomic clone ASV12806.fwd, genomic survey sequence.
ACCESSION CL528379
VERSION CL528379.1 GI:47421590
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 80)
Mitchell,R.S., Belzcel, B.F., Schroder,A.R.W., Shinn,P., Chen,H., Berry,C.C., Ecker,J.R. and Bushman,F.
Retroviral DNA integration: ASLV, HIV and MLV Show Distinct Target Site Preferences
Unpublished (2004)
Contact: Frederic Bushman
Salk Institute Infectious Disease Laboratory
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1630
Fax: 858 554 0341
Email: bushman@salk.edu
Class: PCR with specific primers.
Location/Qualifiers
1..80
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="ASV12806.fwd"
/clone_lib="ASLV-vector integration sites in human 293T-TVA cells"
/note="Human 293T cells expressing the subgroup A avian retrovirus receptor (293T-TVA) were infected with an ASLV-based vector. DNA was isolated and cleaved with restriction enzymes; linkers were ligated onto the cleaved DNA and DNAs were amplified using one primer that bound to the linker DNA and one that bound to the ASLV cDNA. Junctions between integrated ASLV proviruses and cellular DNA were cloned and sequenced."

ORIGIN

Query Match 62.0%; Score 12.4; DB 10; Length 80;
Best Local Similarity 92.9%; Pred. No. 1.2e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TATGGAATGATACC 15
|||
80 TAGGGAATGATACC 67

FEATURES
source

RESULT 24
LOCUS CL656659 70 bp DNA linear GSS 09-JUL-2004
DEFINITION PRI0127a H08 - PRI0127a.B1 (70) Mixed stage fosmid library of P. pacificus var. California *Pristionchus pacificus* genomic, genomic survey sequence.
ACCESSION CL656659.1 GI:50137318
VERSION CL656659.1
KEYWORDS *Pristionchus pacificus*
SOURCE *Pristionchus pacificus*
ORGANISM *Pristionchus pacificus*
REFERENCE Bukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida; Neeidiplogasteridae; *Pristionchus*.
AUTHORS Srinivasan, J., Otto, G. W., Kahlow, U., Geisler, R. and Sommer, R. J.
TITLE 1 (bases 1 to 70)
JOURNAL Appadri: an Acedb database for the nematode satellite organism
PUBMED Nucleic Acids Res. 32 (1), D421-D422 (2004)
COMMENT 1468147
Contact: Sommer RJ
Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
Fax: 00497071601498
Email: ralf.sommer@tuebingen.mpg.de
This library was generated at Caltech, Pasadena, USA and end sequenced at Vancouver, Canada.
Seq primer: T7
Class: fosmid ends.
FEATURES
SOURCE
1..70
Location/Qualifiers
/organism="Pristionchus pacificus"
/mol_type="genomic DNA"
/strain="California"
/db_xref="taxon:54126"
/clone_id="Mixed stage fosmid library of P. pacificus var. California"
/note="Vector: pGifos-5 Fosmid vector"

ORIGIN
Query Match 62.0%; Score 12.4; DB 10; Length 70;
Best Local Similarity 92.9%; Pred. No. 1.1e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 6 GAATGATACCGTCA 19
Db 28 GAATGATACCGCA 41

RESULT 25
LOCUS AZ922984/c 72 bp DNA linear GSS 07-JUN-2002
DEFINITION SUCot5A01 *Sorghum bicolor* SUCot *Sorghum bicolor* genomic similar to *Sorghum bicolor* Retrosor-6 retroelement, genomic survey sequence.
ACCESSION AZ922984
VERSION AZ922984.1 GI:13433205
KEYWORDS GSS.
SOURCE *Sorghum bicolor* (*Sorghum*)
ORGANISM *Sorghum bicolor* (*Sorghum*)
REFERENCE Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; *Sorghum*.
AUTHORS Peterson, D. G., Schulze, S. R., Sciara, E. B., Lee, S. A., Bowers, J. E., Nagel, A., Jiang, N., Tibbitts, D. C., Wesler, S. R. and Peterson, A. H.
TITLE Integration of Cot analysis, DNA cloning, and high-throughput sequencing facilitates genome characterization and gene discovery
JOURNAL Genome Res. 12 (5), 795-807 (2002)
PUBMED 11997346
Contact: Peterson DG
Plant Genome Mapping Laboratory
University of Georgia

Room 162, Riverbend Research Bldg., 110 Riverbend Rd., Athens, GA 30602, USA
Tel: 706-583-0167
Fax: 706-583-0160
Email: dg@arches.uga.edu
Class: Hydroxyapatite-fractionated DNA.
FEATURES
SOURCE
1..72
Location/Qualifiers
/organism="Sorghum bicolor"
/mol_type="genomic DNA"
/cultivar="BTx623"
/db_xref="taxon:4558"
/tissue_type="leaves"
/dev_stage="seedling"
/clone_id="Sorghum bicolor SUCot"
/note="Vector: pGEM-TA-Basy; A Cot analysis was performed for the sorghum genome. Based on the resulting Cot curve, hydroxyapatite chromatography was used to isolate 'highly-repetitive' (HR), 'moderately-repetitive' (MR), and 'single/low-copy' (SL) sequence components from shared genomic DNA. The three repetition-based DNA components were cloned into E. coli to produce HRCot, MRCot, and SUCot genomic libraries. Blotting and sequencing data indicates that each library is representative of the component from which it was derived. Putative ID listings given for sequences are based on comparison (blastn) with sequences in the NCBI Nr Database. Only the primary match is given (all primary E values are < or = 1.00E-5). In no instance does a 'Cot clone' contain the complete sequence of its putative Nr match."

ORIGIN
Query Match 62.0%; Score 12.4; DB 9; Length 72;
Best Local Similarity 92.9%; Pred. No. 1.1e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 4 TGGATGATACCGT 17
Db 63 TGAATGATACCGT 50

RESULT 26
LOCUS AZ922992/c 72 bp DNA linear GSS 07-JUN-2002
DEFINITION SUCot5C05 *Sorghum bicolor* SUCot *Sorghum bicolor* genomic similar to *Sorghum bicolor* Retrosor-6 retroelement, genomic survey sequence.
ACCESSION AZ922992
VERSION AZ922992.1 GI:13433213
KEYWORDS GSS.
SOURCE *Sorghum bicolor* (*Sorghum*)
ORGANISM *Sorghum bicolor* (*Sorghum*)
REFERENCE Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; *Sorghum*.
AUTHORS Peterson, D. G., Schulze, S. R., Sciara, E. B., Lee, S. A., Bowers, J. E., Nagel, A., Jiang, N., Tibbitts, D. C., Wesler, S. R. and Peterson, A. H.
TITLE Integration of Cot analysis, DNA cloning, and high-throughput sequencing facilitates genome characterization and gene discovery
JOURNAL Genome Res. 12 (5), 795-807 (2002)
PUBMED 11997346
Contact: Peterson DG
Plant Genome Mapping Laboratory
University of Georgia
Room 162, Riverbend Research Bldg., 110 Riverbend Rd., Athens, GA 30602, USA
Tel: 706-583-0167
Fax: 706-583-0160
Email: dg@arches.uga.edu
Class: Hydroxyapatite-fractionated DNA.
FEATURES
SOURCE
1..72
Location/Qualifiers


```

REFERENCE          3 (bases 1 to 58)
AUTHORS            Genoscope.
TITLE              Direct Submission
JOURNAL            Submitted (12-APR-2000) Genoscope - Centre National de Sequencage :
                   BP 191 91006 Evry cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
COMMENT            Web : www.genoscope.cns.fr)
                   This sequence is a single read and was generated as part of a large
                   scale clone-end sequencing project of the Tetraodon nigroviridis
                   genome. For more information, please take a look at
                   http://www.genoscope.cns.fr/tetraodon.
FEATURES           Location/Qualifiers
source             1..58
                  /organism="Tetraodon nigroviridis"
                  /mol_type="genomic DNA"
                  /db_xref="taxon:99883"
                  /clone="012FF21"
                  /clone_1lb="G"
                  /note="Genoscope sequence ID : COBG012CC11LP1
                   end : T7"

ORIGIN
Query Match      63.0% ; Score 12.6; DB 11; Length 58;
Best Local Similarity 78.9% ; Pred. No. 8.7e+04;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy               1 TTATGAATGATTACCGTCA 19
                 ||||||| ||||| ||
Db               37 TTTTGAGAGAACCACGACA 19

RESULT 22
CO745042/c       63 bp mRNA linear EST 30-JUL-2004
DEFINITION       TGSTZYP25g10.y2 Tg CAsr Tachyzoite cDNA Library 2 Toxoplasma
VERSION          gondii cDNA clone TGSTZyp25g10.y2 5', mRNA sequence.
ACCESSION        CO745042
KEYWORDS         CO745042.1 GI:50858573
SOURCE           EST.
ORGANISM         Toxoplasma gondii
                Tokoplasmata
                Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
                Sarcocystidae; Toxoplasma.
REFERENCE        1 (bases 1 to 63)
AUTHORS          Tang,K., Cole,R.R., Fogarty,S., Sibley,L.D., Ajijoka,J.A., White,M.,
                Clifton,S., Page,D., Martin,J., Wylie,T., Dante,M., Marra,M.,
                Hillier,L., Kucaba,D., Theising,B., Bowers,Y., Gibbons,M.,
                Riter,E., Bennett,J., Franklin,C., Tsagarisvili,R., Ronko,I.,
                Kennedy,S., Maguire,L., Waterston,R. and Wilson,R.
TITLE            Toxoplasma EST Project
JOURNAL          Unpublished (2001)
COMMENT          Contact: Clifton, S.
                  Toxoplasma EST Project
                  Washington University School of Medicine
                  4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
                  Tel.: 314 286 1800
                  Fax: 314 286 1810
                  Email: toxo@watson.wustl.edu
                  Contact David Sibley (toxoset@orcim.wustl.edu) for further
                  information relating to organism, libraries, or clone availability
                  Putative full length read
                  vector to vector length is
                  Seq primer: T7 from Gibco.
FEATURES         Location/Qualifiers
source           1..63
                /organism="Toxoplasma gondii"
                /mol_type="mRNA"
                /db_xref="taxon:5811"
                /clone="TGSTZYP25g10.y2"
                /dev_stage="Tachyzoite"
                /lab_host="C610"
                /clone_1lb="Tg CAsr Tachyzoite cDNA Library 2"
                /note="Vector: pDNR-LTB; Site 1: SfII; Site 2: SfII; The
                  cDNA library was constructed by Kelian Tang, and Robert

```

ORIGIN	Query Match		63.0%;	Score 12.6;	DB 7;	Length 63;	
	Best Local Similarity		75.0%;	Pred. No. 8.8e+04;			
	Matches	15;	Conservative	0;	Mismatches	5;	Indels 0; Gaps 0;
QY	1		TTATGAGTATGATACCGTCAT	20			
DB	33		TTAAGAGATGATACCGTCAT	14			
RESULT 23							
LOCUS	CG529309/c	74 bp	mRNA	linear	GSS 01-OCT-2003		
DEFINITION	CG529309.1 Mus musculus 129SV/Ev Mus musculus CDNA clone OSTR109611, mRNA sequence.						
ACCESSION	CG529309						
VERSION	CG529309.1	GI:37315881					
KEYWORDS	GSS.						
SOURCE	Mus musculus (house mouse)						
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidae; Muridae; Mus.						
REFERENCE	1 (bases 1 to 74)						
AUTHORS	Zambrowicz, B.P., Aduin, A., Ramirez-Solis, R., Richter, L.J., Piggett, J., Beltrande-Rio, H., Buxton, E.C., Edwards, J., Finch, R.A., Friddle, C.J., Gupta, A., Hansen, G., Hu, Y., Huang, W., Jaijng, C., Key, B.W., Jr., Kipp, P., Kohlhauff, B., Ma, Z.-Q., Markesich, D., Payne, R., Potter, D.G., Qian, N., Shaw, J., Schrick, J., Shi, Z.-Z., Sparks, M.J., Van Sligtenhorst, I., Vogel, P., Walke, W., Xu, N., Zhu, Q., Person, C. and Sands, A.T.						
TITLE	Mnrl kinase deficiency lowers blood pressure in mice: a gene-trap screen to identify potential targets for therapeutic intervention						
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)						
PUBMED	14610273						
COMMENT	Contact: Zambrowicz BP OmniBank Lexicon Genetics Incorporated 4000 Research Forest Drive, The Woodlands, TX 77381, USA Email: materials@lexgen.com Gene trap sequence tag generated by 3' RACE from mouse ES cells as described in Zambrowicz et al (Nature, 1998 Apr 9;392(6676):608-11) Class: Gene Trap.						
FEATURES	location/Qualifiers						
source	1..74						
	/organism="Mus musculus"						
	/mol_type="mRNA"						
	/strain="129SV/Ev"						
	/db_xref="taxon:10090"						
	/clone="OSTR109611"						
	/cell_type="embryonic stem cell"						
	/clone_lib="Mus musculus 129SV/Ev"						
ORIGIN							
	Query Match						
	Best Local Similarity						
	Matches	15;	Conservative	0;	Mismatches	4;	Indels 0; Gaps 0;
QY	1		TTATGAGTATGATACCGTCAT	19			
DB	21		TTATGATCTCATACCGTCAT	3			

JOURNAL
PUBMED
12874060
REFERENCE
AUTHORS
2
Rosso,M.G., Li.Y., Strizhov,N., Reies,B., Dekker,K. and
Weishaar,B.
TITLE
An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for
flanking sequence tag-based reverse genetics
JOURNAL
PUBMED
14756321
REFERENCE
AUTHORS
3
Strizhov,N., Li.Y., Rosso,M.G., Viehoveer,P., Dekker,K.A. and
Weishaar,B.
TITLE
High-throughput generation of sequence indexes from T-DNA
mutagenized Arabidopsis thaliana lines
JOURNAL
PUBMED
14682050
REFERENCE
AUTHORS
4
Rosso,M.G., Strizhov,N., Li.Y. and Weishaar,B.
TITLE
Direct Submission
COMMENT
Submitted (31-MAR-2004) Weishaar B., Max-Planck-Institut fuer
Zuechtungsforchung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
This sequence has been recovered from the left border of the T-DNA.
It indicates an insertion close to or within gene At5g65020.
Details on the protocols used for generation of the sequence are
described in References 1-3. The sequences are generated at the MPI
for Plant Breeding Research in the context of the GABI-Kat project.
GABI-Kat is part of the German Plant Genomics program designated
'GABI'. Information on line availability can be found at:
<http://www.mpiz-koeln.mpg.de/GABI-Kat/>.
Location/Qualifiers
1. .52
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/db_xref="taxon:3702"
/clone="GK-166H08-013361"
/clone_1lb="Arabidopsis thaliana T-DNA insertion lines"
/ecotype="Col-0"
/note="PCR was performed on DNA from Arabidopsis thaliana
plants (T1) which were transformed with the T-DNA from
vector PAC161 (Genbank accession number: AJ537514). The
lines contain one or more T-DNA insertions. The DNA
fragment(s) resulting from the PCR were directly sequenced
to determine the genomic sequence flanking the insertion.
T-DNA derived sequences were removed."

ORIGIN
Query Match 63.0%; Score 12.6; DB 10; Length 52;
Best Local Similarity 78.9%; Pred. No. 8.6e+04;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY
1 TTATGGAATGATACCGTCA 19
23 TTATGGAATGATACCGCTTA 41

RESULT 20
AJ587959/c
LOCUS
DEFINITION
58 bp DNA linear GSS 15-JAN-2004
Arabidopsis thaliana T-DNA flanking sequence, left border, clone
345C03, genomic survey sequence.
ACCESSION
AJ587959
VERSION
AJ587959.1 GI:37937583
KEYWORDS
GSS; left border; T-DNA flanking sequence.
SOURCE
Arabidopsis thaliana (thale cress)
ORGANISM
Arabidopsis thaliana
REFERENCE
AUTHORS
1
Brunaud,V., Balzerque,S., Dubreucq,B., Aubourg,S., Samson,F.,
Chauvin,S., Bechtold,N., Crnaud,C., DeRose,R., Pelletier,G.,
Lepointec,L., Caboche,M. and Lecharny,A.

TITLE
T-DNA integration into the Arabidopsis genome depends on sequences
of pre-insertion sites
JOURNAL
PUBMED
12446565
REFERENCE
AUTHORS
2
Balzerque,S.
TITLE
Direct Submission
COMMENT
Submitted (23-OCT-2003) Balzerque S., UMRGV, INRA/CNRS, 2 rue
Gaston Cremieux, 91057 Evry cedex, FRANCE
PCR was performed on DNA from transformants of Arabidopsis thaliana
plants from INRA (Versailles). The DNA fragment(s) resulting from
the PCR were directly sequenced from the left or the right border
to determine the genomic sequence flanking the insertion. T-DNA
derived sequences were removed. Information to order the
corresponding mutant line and a link to a database providing a
graphical display of the insertion site are available at
<http://dbsgpp.versailles.inra.fr/publiclines/>. This sequence has
been generated in the framework of the French plant genomics
program 'Genoplante' (<http://www.genoplante.com> and
<http://genoplante-info.infbioingen.fr>).
Location/Qualifiers
1. .58
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/db_xref="taxon:3702"
/clone="345C03"
/clone_1lb="Arabidopsis thaliana T-DNA insertion lines"
/ecotype="Massilewskija"
/note="T-DNA flanking sequence
left border"

ORIGIN
misc_feature
Query Match 63.0%; Score 12.6; DB 10; Length 58;
Best Local Similarity 78.9%; Pred. No. 8.7e+04;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY
2 TATGGAATGATACCGTCAT 20
21 TATGGAATGATACCGTCAT 3

RESULT 21
CNS03BOT/c
LOCUS
DEFINITION
58 bp DNA linear GSS 01-SEP-2000
Tetradon nigroviridis genome survey sequence T7 end of clone
012F21 of library G from Tetradon nigroviridis, genomic survey
sequence.
ACCESSION
AL236774
VERSION
AL236774.1 GI:7895909
KEYWORDS
GSS; genome survey sequence.
SOURCE
Tetradon nigroviridis
ORGANISM
Tetradon nigroviridis
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontidae; Tetraodontidae; Tetradon.

REFERENCE
AUTHORS
1
Roest Crolius,H., Jallion,O., Dasilva,C., Bouneau,L., Fisher,C.,
Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
Saurin,W. and Weissenbach,J.
TITLE
Estimate of human gene number provided by genome-wide analysis
using Tetradon nigroviridis DNA sequence
JOURNAL
PUBMED
10835645
REFERENCE
AUTHORS
2
Roest Crolius,H., Jallion,O., Dasilva,C., Ozouf-Costaz,C.,
Fizames,C., Fischer,C., Bouneau,L., Billault,A., Quetier,F.,
Saurin,W., Bernot,A. and Weissenbach,J.
TITLE
Characterization and repeat analysis of the compact genome of the
freshwater pufferfish Tetradon nigroviridis
JOURNAL
PUBMED
10899143

REFERENCE
1 (bases 1 to 40)
Satoch,N., Satoch,Y., Kohara,Y. and Shin-I,T.
Expressed genes in *Ciona intestinalis*
JOURNAL
Unpublished (2000)
COMMENT
Contact: Nori Satoch
Department of Zoology
Kyoto University
Sakyo-ku, Kyoto 606-8502, Japan
Tel: 81-75-753-4081
Fax: 81-75-705-1113
Email: satoch@acidian.zool.kyoto-u.ac.jp.

FEATURES
Source
1..40
/organism="Ciona intestinalis"
/mol_type="mRNA"
/db_xref="taxon:7719"
/clone="c1eg24k14"
/tissue_type="whole animal"
/dev_stage="egg"
/clone_lib="Nori Satoch unpublished cDNA library, egg"

ORIGIN
Query Match 63.0%; Score 12.6; DB 1; Length 40;
Best Local Similarity 75.0%; Pred. No. 8.4e+04;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Oy 1 TTATGATGATACCGTCAT 20
|||||
Db 13 TTATGATCAACACACAT 32
|||||

RESULT 17
LOCUS BX193212 44 bp DNA linear GSS 28-JAN-2003
DEFINITION *Danio rerio* genomic clone DKEX-204N22, genomic survey sequence.
ACCESSION BX193212
VERSION BX193212.1 GI:28025098
KEYWORDS GSS.
SOURCE *Danio rerio* (zebrafish)
ORGANISM *Danio rerio*
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; *Danio*.
1 (bases 1 to 44)
Humphrey,S.J., Huckle,E. and Durham,J.L.
Direct Submission
Submitted (27-JAN-2003) The Sanger Institute, Wellcome Trust Genome
Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humphrey@sanger.ac.uk Unpublished
This sequence was generated from the SP6 end of BAC 204N22. 204N22
is part of the Daniokey BAC library created by R. Plaetke and N.V.
Keygene. Further details:
http://www.sanger.ac.uk/Projects/D_rerio/
Location/Qualifiers

FEATURES
Source
1..44
/organism="Danio rerio"
/mol_type="genomic DNA"
/db_xref="taxon:7955"
/clone="DKEX-204N22"
/tissue_type="Testis"
/note="vector pindigobAC-536"

COMMENT
Query Match 63.0%; Score 12.6; DB 10; Length 44;
Best Local Similarity 78.9%; Pred. No. 8.4e+04;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

ORIGIN
Query Match 63.0%; Score 12.6; DB 10; Length 44;
Best Local Similarity 78.9%; Pred. No. 8.4e+04;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 1 TTATGATGATACCGTCAT 19
|||||
Db 3 TTATGATGATGACGATTA 21
|||||

RESULT 18
LOCUS BZ289135/c 52 bp DNA linear GSS 24-OCT-2002
DEFINITION *Salik* 022532.47.40.x *Arabidopsis thaliana* TDNA insertion lines
survey sequence.
COMMENT
Survey sequence.
ACCESSION BZ289135
VERSION BZ289135.1 GI:24330411
KEYWORDS GSS.
SOURCE *Arabidopsis thaliana* (thale cress)
ORGANISM *Arabidopsis thaliana*
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; *Arabidopsis*.
1 (bases 1 to 52)
Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
Gadrial,B.C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
Shim,P., Zimmerman,J. and Ecker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the
Arabidopsis Genome
Unpublished (2001)
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (Signal)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of
TDNA.
Class: TDNA tagged.
Location/Qualifiers

FEATURES
Source
1..52
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/ecotype="Col-0"
/db_xref="taxon:3702"
/clone="SALK_022532.47.40.x"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"

ORIGIN
Query Match 63.0%; Score 12.6; DB 9; Length 52;
Best Local Similarity 78.9%; Pred. No. 8.6e+04;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 2 TATGATGATACCGTCAT 20
|||||
Db 40 TATGATATACACCATGAT 22
|||||

RESULT 19
LOCUS AL759243 52 bp DNA linear GSS 01-APR-2004
DEFINITION *Arabidopsis thaliana* T-DNA flanking sequence GK-16H08-013361,
genomic survey sequence.
ACCESSION AL759243
VERSION AL759243.1 GI:21497591
KEYWORDS GSS.
SOURCE *Arabidopsis thaliana* (thale cress)
ORGANISM *Arabidopsis thaliana*
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; *Arabidopsis*.
1
Li,Y., Rosso,M.G., Strizhov,N., Viehoveer,P. and Weisshaar,B.
Gabi-Kat SimpleSearch: a flanking sequence tag (FST) database for
the identification of T-DNA insertion mutants in *Arabidopsis*

ORIGIN
Query Match 63.0%; Score 12.6; DB 9; Length 52;
Best Local Similarity 78.9%; Pred. No. 8.6e+04;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

ORIGIN
Query Match 63.0%; Score 12.6; DB 9; Length 52;
Best Local Similarity 78.9%; Pred. No. 8.6e+04;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

REFERENCE
Li,Y., Rosso,M.G., Strizhov,N., Viehoveer,P. and Weisshaar,B.
Gabi-Kat SimpleSearch: a flanking sequence tag (FST) database for
the identification of T-DNA insertion mutants in *Arabidopsis*

p1rbetago gene trap. Sequence tag generated by 5'RACE. Additional sequence information can be found at:
'http://genetrapp.gsf.de/project/web_new/database/result_clone.html?clone_id=A036B06' ES cell line harboring insertion mutation of target gene is available at:
'http://genetrapp.gsf.de/project/web_new/order_clones/howtoorder.htm'
1' Inhouse Sequence Identifier: 09227
Class: Gene Trap.

FEATURES
source

1..76
Location/Qualifiers
/organism="Mus musculus"
/mol_type="mRNA"
/strain="129 Sv"
/db_xref="taxon:10090"
/clone="A036B06"
/sex="Male"
/cell_type="Embryonic stem cell"
/cell_line="ES cells 129S2 (formerly 129/SvPas)"
/clone_id="G8TC Gene Trap Library GV03C04"
/note="Vector: p1rbetago"

ORIGIN

Query Match 64.0%; Score 12.8; DB 10; Length 76;
Best Local Similarity 87.5%; Pred. No. 7e+04; Mismatches 2; Indels 0; Gaps 0;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 GGAATGATACCGTCAT 20
|||||
Db 25 GGAATGATGACGTGAT 10

RESULT 14
CG515614/c 77 bp mRNA linear GSS 01-OCT-2003
LOCUS OST71843 Mus musculus 129Sv/Ev Mus musculus cDNA clone OST71843,
DEFINITION mRNA sequence.
ACCESSION CG515614 GI:37302187
VERSION CG515614.1
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 77)
Zambrowicz,B.P., Abuin,A., Ramirez-Solis,R., Richter,L.J.,
Piggott,J., BeltrandeRio,H., Buxton,E.C., Edwards,J., Finch,R.A.,
Fridde,C.J., Gupta,A., Hansen,G., Hu,Y., Huang,W., Jaling,C.,
Key,B.W., Jr., Kipp,P., Kohlhauff,B., Ma,Z.-Q., Markesich,D.,
Payne,R., Potter,D.G., Qian,N., Shaw,J., Schrick,J., Shi,Z.-Z.,
Sparks,M.J., Van Sligtenhorst,I., Vogel,P., Walke,W., Xu,N.,
Zhu,Q., Person,C. and Sands,A.T.

Wnk1 kinase deficiency lowers blood pressure in mice: a gene-trap screen to identify potential targets for therapeutic intervention
Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)
14610273
Contact: Zambrowicz BP
Omnibank

lexicon Genetics Incorporated
4000 Research Forest Drive, The Woodlands, TX 77381, USA
Email: materials@lexgen.com
Gene trap sequence tag generated by 3' RACE from mouse ES cells as described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)
Class: Gene Trap.

FEATURES
source

1..77
Location/Qualifiers
/organism="Mus musculus"
/mol_type="mRNA"
/strain="129Sv/Ev"
/db_xref="taxon:10090"
/clone="OST71843"
/cell_type="embryonic stem cell"
/clone_id="Mus musculus 129Sv/Ev"

ORIGIN

Query Match 64.0%; Score 12.8; DB 10; Length 77;
Best Local Similarity 82.4%; Pred. No. 7e+04; Mismatches 3; Indels 0; Gaps 0;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4 TGAATGATACCGTCAT 20
|||||
Db 29 TGAATGATGACGTGAT 13

RESULT 15
TA137C05Q 39 bp DNA linear GSS 13-DEC-2000
LOCUS T. brucei sheared genomic DNA clone 137c05, reverse sequence,
DEFINITION genomic survey sequence.
ACCESSION AL466263
VERSION AL466263.1 GI:11835618
KEYWORDS GSS.
SOURCE Trypanosoma brucei
ORGANISM Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma.
1 (bases 1 to 39)
Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
Melville,S.B., Rajadream,M.A. and Barrell,B.G.
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and nhl@sanger.ac.uk

COMMENT

Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).
Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/T_brucei/.

FEATURES
source

1..39
Location/Qualifiers
/organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="137c05"

ORIGIN

Query Match 63.0%; Score 12.6; DB 11; Length 39;
Best Local Similarity 78.9%; Pred. No. 8.3e+04; Mismatches 4; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 TATGATGATACCGTCAT 20
|||||
Db 15 TGTGGGTATGATACCTTCAT 33

RESULT 16
AV963579 40 bp mRNA linear EST 14-MAR-2002
LOCUS AV963579 Nori Satoh unpublished cDNA library, egg Clona
DEFINITION intestinalis cDNA clone c1eg24K14 5', mRNA sequence.
ACCESSION AV963579
VERSION AV963579.1 GI:19451878
KEYWORDS EST.
SOURCE Clona intestinalis
ORGANISM Clona intestinalis
Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;

ORIGIN and selected for ampicillin resistance."

Query Match 66.0%; Score 13.2; DB 9; Length 48;
Best Local Similarity 83.3%; Pred. No. 4.1e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 TATGGAATGATACCGTCA 19
| | | | | | | | | | | | | | | | | | | | |
Db 3 TGTGGATGATACCTGTCA 20

RESULT 6 CN924691 65 bp mRNA linear EST 07-JUN-2004
LOCUS CN924691 domestic cDNA clone AELA008223, mRNA sequence.
DEFINITION CN924691
VERSION CN924691.1 GI:48397504
KEYWORDS
SOURCE
ORGANISM Malus x domestica

REFERENCE 1 (bases 1 to 65)
AUTHORS Beuning, L., Bowen, J., Crowhurst, R., Gleave, A., Janssen, B.,
McCarthy, S., Newcomb, R., Ross, G., Snowden, K., Walton, E. and Yauk, Y.
TITLE HortResearch Apple EST Project
JOURNAL Unpublished (2004)
COMMENT Contact: Gleave, A.
Sequencing Facility
The Horticulture and Food Research Institute of New Zealand Ltd
120 Mt Albert Rd, Mt Albert, Auckland, New Zealand
Tel: 00 64 09 815 4200
Fax: 00 64 09 815 4201
Email: est@hortresearch.co.nz.

FEATURES
source
1..65
Location/Qualifiers

/organism="Malus x domestica"
/mol_type="mRNA"
/db_xref="taxon:3750"
/clone="AELA008223"
/tissue_type="leaf"
/dev_stage="Young, expanding"
/clone_1lb="(AELA) Royal Gala young expanding leaf"
/note="Vector: pBK-CMV; Library sequenced by Genesis Research & Development"

ORIGIN
Query Match 66.0%; Score 13.2; DB 7; Length 65;
Best Local Similarity 83.3%; Pred. No. 4.2e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 TATGGAATGATACCGTCA 19
| | | | | | | | | | | | | | | | | | | | |
Db 48 TGTGGATGATACAGTCA 65

RESULT 7
LOCUS C2486525 72 bp DNA linear GSS 29-APR-2005
DEFINITION f03919-5prime Exelixis piggyBac WH insertions Drosophila melanogaster genomic Sequence recovered from 5' end of piggyBac, genomic survey sequence.
ACCESSION C2486525
VERSION C2486525.1 GI:629833963
KEYWORDS GSS.
SOURCE Drosophila melanogaster (fruit fly)
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

REFERENCE 1 (bases 1 to 72)

AUTHORS Thibault, S.T., Singer, M.A., Miyazaki, M.Y., Milash, B., Dompe, N.A.,
Singh, C.M., Buchholz, R., Demsky, M., Fawcett, R., Francis-Lang, H.L.,
Ryner, L., Cheung, L.M., Chong, A., Erickson, C., Fisher, W.W.,
Greer, K., Harcourt, S.R., Howie, E., Jakkula, L., Joo, D., Killpack, K.,
Lauffer, A., Mazotta, J., Smith, R.D., Stevens, L.M., Stuber, C.,
Tan, L.R., Ventura, R., Woo, A., Zakrajsek, I., Zhao, L., Chen, F.,
Swimmer, C., Koczynski, C., Duyk, G., Winberg, M.L. and Margolis, J.
A complementary transposon tool kit for Drosophila melanogaster
using P and piggyBac
Nat. Genet. 36 (3), 283-287 (2004)

TITLE
JOURNAL PUBMED
COMMENT Contact: Roger A Hoskins
Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory
Mailstop 64-121, One Cyclotron Road, Berkeley, CA 94720, USA
Tel: 510 486 4015
Fax: 510 486 6798
Email: Rhoekins@lbl.gov

Sequence recovery method was inverse PCR.
Sequence orientation is forward strand relative to 5' end of
piggyBac element.
The piggyBac insertion position is 69 in the 72 bases. This
insertion position refers to the first base of the 4 base TTAA
target recognition sequence.
Class: transposon insertion site.
Location/Qualifiers

FEATURES
source
1..72
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/strain="isogenic w- strain"
/db_xref="taxon:7227"
/clone_1lb="Exelixis piggyBac WH insertions"
/note="Vector: piggyBac WH (Genbank accession number
AY15148); An isogenic w- Drosophila melanogaster strain
was mutagenized by remobilization of transposable
elements. We remobilized the WH element using the
constitutive alpha-1-tubulin-piggyBac transposase source.
We remobilized the WH element from a single ammunition
element on the Binsincy balancer chromosome in dysgenic
females. We outcrossed dysgenic virgin females in vials to
the isogenic w- strain and selected new hops in the
following generation. All lines were mapped to a
chromosome by standard genetic methods, examined for
homozygous viability, and used for recovery of flanking
genomic sequence by inverse PCR."

ORIGIN

Query Match 66.0%; Score 13.2; DB 10; Length 72;
Best Local Similarity 83.3%; Pred. No. 4.3e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 TTATGGAATGATACCGTC 18
| | | | | | | | | | | | | | | | | | | | |
Db 32 TTATGGCATTAATTCGTC 15

RESULT 8
LOCUS CM382475 77 bp DNA linear GSS 01-NOV-2004
DEFINITION f5b001f064h09f0 Sorghum methylation filtered library (LibID: 104)
Sorghum bicolor genomic clone f5b001f064h09, genomic survey
sequence.
ACCESSION CM382475
VERSION CM382475.1 GI:55100919
KEYWORDS GSS.
SOURCE Sorghum bicolor (sorghum)
ORGANISM Sorghum bicolor
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACAD
clade; Panicoideae; Andropogoneae; Sorghum.
REFERENCE 1 (bases 1 to 77)
Bedell, J.A., Budiman, M.A., Nunberg, A., Citek, R.W., Robbins, D.,

ORIGIN

Query Match 68.0%; Score 13.6; DB 9; Length 64;
Best Local Similarity 80.0%; Pred. No. 2.6e+04;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

1 TTATGGATGATACCGTCAT 20
47 TTATGAGATGAGCGTCAT 28

/sex="Male"
/lab_host="E. Coli strain X110-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGCGIM library"
/note="Vector: pMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli X110-Gold (Stratagene) cells and selected for ampicillin resistance."

RESULT 4
TA374D04P 70 bp DNA linear GSS 13-DEC-2000
LOCUS T. brucei sheared genomic DNA clone 374d04, forward sequence,
DEFINITION genomic survey sequence.
ACCESSION AL495665
VERSION AL495665.1 GI:11873081
KEYWORDS GSS.
SOURCE Trypanosoma brucei
ORGANISM Trypanosoma brucei
Eukaryota; Euzlenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma.
1 (bases 1 to 70)
Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,
Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
Melville, S.E., Rajandream, M.A. and Barrell, B.G.
Direct Submission
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
nilesanger.ac.uk
COMMENT Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
to give a tight size distribution (4 kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaundin and B.
Barrell, Oxford University Press, 1999).
Email: nilesanger@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.

FEATURES
source
1..70
/organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="374d04"

ORIGIN

Query Match 68.0%; Score 13.6; DB 11; Length 70;
Best Local Similarity 80.0%; Pred. No. 2.6e+04;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

1 TTATGGATGATACCGTCAT 20
9 TTGTGGATGATCCCAACAT 28

RESULT 5
AZ797513 48 bp DNA linear GSS 16-FEB-2001
LOCUS 2M0053H15R Mouse 10kb plasmid UGCGIM library Mus musculus genomic
DEFINITION clone UGCGCM0053H15 R, genomic survey sequence.
ACCESSION AZ797513
VERSION AZ797513.1 GI:12946668
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Murioidea; Muridae; Murinae; Mus.
1 (bases 1 to 48)
Islam, H., Longacre, S., Mahmoud, M., Meenen, F., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 1000 Std Error: 0.00
Plate: 0053 row: H column: 15
Seq primer: CACACGAGAAACGCTATGACC
Class: plasmid ends
High quality sequence scop: 48.
location/Qualifiers
1..48
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCGCM0053H15"
/sex="Male"
/lab_host="E. Coli strain X110-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGCGIM library"
/note="Vector: pMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli X110-Gold (Stratagene) cells

FEATURES
source

1..48
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCGCM0053H15"
/sex="Male"
/lab_host="E. Coli strain X110-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGCGIM library"
/note="Vector: pMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli X110-Gold (Stratagene) cells

c 96	11.6	58.0	40	6	CF329665	CF329665 NACL--05-
c 97	11.6	58.0	41	10	AG206339	AG206339 Oryza sat
c 98	11.6	58.0	50	10	AG189033	AG189033 Pan trogl
c 99	11.6	58.0	53	11	CR357573	CR357573 Arabidops
c 100	11.6	58.0	53	11	HSMC24C02	X88257 H.sapiens D

ALIGNMENTS

RESULT 1
CG530112/c 73 bp mRNA linear GSS 01-OCT-2003
LOCUS OST111465 Mus musculus 1295v/Ev Mus musculus cDNA clone OST11465,
DEFINITION mRNA sequence.

ACCESSION CG530112
VERSION CG530112
KEYWORDS GI:37316684
SOURCE GSS.
ORGANISM Mus musculus (house mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 73)
AUTHORS Zambrowicz,B.P., Abuin,A., Ramirez-Solis,R., Richter,L.U.,
Piggett,J., BeltrandeRio,H., Buxton,E.C., Edwards,J., Finch,R.A.,
Fridde,C.J., Gupta,A., Hansen,G., Hu,Y., Huang,C.,
Key,B.W., Jr., Klipp,P., Kohhauff,B., Ma,Z.-Q., Markesich,D.,
Payne,R., Porter,D.C., Qian,N., Shaw,J., Schrick,J., Shi,Z.-Z.,
Sparkes,M.J., Van Sligtenhorst,I., Vogel,P., Walke,W., Xu,N.,
Zhu,Q., Person,C. and Sande,A.T.
TITLE Mnk1 kinase deficiency lowers blood pressure in mice: a gene-trap
screen to identify potential targets for therapeutic intervention
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)
PUBMED 14610273
COMMENT Contact: Zambrowicz BP
OmniBank
Lexicon Genetics Incorporated
4000 Research Forest Drive, The Woodlands, TX 77381, USA
Email: material@lexgen.com
Gene trap sequence tag generated by 3' RACE from mouse ES cells as
described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)
Class: Gene trap.

FEATURES
source Location/Qualifiers
1..73
/organism="Mus musculus"
/mol_type="mRNA"
/strain="129Sv/Ev"
/db_xref="taxon:10090"
/clone="OST11465"
/cell_type="embryonic stem cell"
/clone_lib="Mus musculus 129Sv/Ev"

ORIGIN

Query Match 79.0%; Score 15.8; DB 10; Length 73;
Best Local Similarity 85.0%; Pred. No. 1.7e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TTATGATGATACCGTCAT 20
DB 43 TTATGATGATACCGTCAT 24

RESULT 2
LOCUS BM510050 79 bp mRNA linear EST 30-AUG-2004
DEFINITION BM510050 Yutaka Satou beta-catenin downstream gene enriched cDNA
library Clona savigny1 cDNA clone csbt001d09, mRNA sequence.
ACCESSION BM510050
VERSION BM510050.1 GI:51671748
KEYWORDS EST.
SOURCE Clona savigny1
ORGANISM Clona savigny1

REFERENCE 1 (bases 1 to 79)
AUTHORS Imai,K.S., Satoh,N. and Satou,Y.
TITLE Expressed genes in Clona savigny1 (Imai, Satoh, Satou)
JOURNAL Unpublished (2004)
COMMENT Contact: Yutaka Satou
Department of Zoology
Kyoto University
Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
Tel: 81-75-753-4095
Fax: 81-75-705-1113
Email: yutaka@scidian.zool.kyoto-u.ac.jp.
Location/Qualifiers

FEATURES
source
1..79
/organism="Clona savigny1"
/mol_type="mRNA"
/db_xref="taxon:51511"
/clone="csbt001d09"
/clone_lib="Yutaka Satou beta-catenin downstream gene
enriched cDNA library"

ORIGIN

Query Match 69.0%; Score 13.8; DB 5; Length 79;
Best Local Similarity 75.0%; Pred. No. 2.1e+04;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 TTATGATGATACCGTCAT 20
DB 42 TTATGATGATACCGTCAT 61

RESULT 3
A2474062/c 64 bp DNA linear GSS 04-OCT-2000
LOCUS IM0290M14F Mouse 10kb plasmid UGCM library Mus musculus genomic
DEFINITION clone UGCM0290M14 F, genomic survey sequence.
ACCESSION A2474062
VERSION A2474062.1 GI:10632187
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 64)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamli,C.,
Isiam,H., Longacre,S., Mahmoud,M., Meenen,B., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: dunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0290 row: M column: 14
Seq primer: CGTGTAAACGACGCGCAGT
Class: plasmid ends
High quality sequence atp: 64.
Location/Qualifiers

FEATURES
source
1..64
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCM0290M14"

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 1, 2006, 22:32:40 ; Search time 2338 Seconds
(without alignments)
318.496 Million cell updates/sec

Title: US-10-653-528-33

Perfect score: 20

Sequence: 1 ttatggaatgataacgctcat 20

Scoring table: IDENTITY NUC

Gapop 10_0 , Gapext 1.0

Searched: 41078325 seqs, 2393541228 residues

Total number of hits satisfying chosen parameters: 512758

Minimum DB seq length: 0
Maximum DB seq length: 80

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_hic:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_est7:*
9: gb_gss1:*
10: gb_gss2:*
11: gb_gss3:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query Match	Length	DB	ID	Description
C 1	15.8	79.0	73	10	CG530112	OST111465	CG530112 OST111465
C 2	13.6	69.0	79	5	BM510050	BM510050	BM510050 BM510050
C 3	13.6	68.0	64	9	AZ474062	IM0290M14	AZ474062 IM0290M14
4	13.6	68.0	70	11	TA374052	AL495665 T. brucei	AL495665 T. brucei
5	13.2	66.0	48	9	AZ797513	2M0053H15	AZ797513 2M0053H15
6	13.2	66.0	65	7	CN924691	000415AEL	CN924691 000415AEL
7	13.2	66.0	72	10	CM382475	f03919-5P	CM382475 f03919-5P
C 8	13.2	66.0	77	10	CM382475	fsbD001f0	CM382475 fsbD001f0
C 9	13.2	66.0	79	10	BM992081	Arabidops	BM992081 Arabidops
C 10	12.8	64.0	49	1	AA985054	AA985054 am69f06.8	AA985054 am69f06.8
C 11	12.8	64.0	57	8	U44189	ENU44189 Ab	U44189 ENU44189 Ab
C 12	12.8	64.0	74	1	AV854960	AV854960	AV854960 AV854960
C 13	12.8	64.0	76	10	CL214052	AO35B06 G	CL214052 AO35B06 G
C 14	12.8	64.0	77	10	CG515614	OST11843	CG515614 OST11843
15	12.6	63.0	39	11	TA137C05Q	AV963579	TA137C05Q AV963579
16	12.6	63.0	40	10	AV963579	AV963579	AV963579 AV963579
17	12.6	63.0	44	10	BM193212	Danio rer	BM193212 Danio rer
C 18	12.6	63.0	52	9	BZ289135	SLK_0225	BZ289135 SLK_0225
C 19	12.6	63.0	52	10	AL759243	Arabidops	AL759243 Arabidops
C 20	12.6	63.0	58	10	AJ587959	Arabidops	AJ587959 Arabidops
C 21	12.6	63.0	58	11	CNS03BOT	AL36774 Tetraodon	AL36774 Tetraodon
C 22	12.6	63.0	63	7	COT45042	TGESTzyp2	COT45042 TGESTzyp2

C 23	12.6	63.0	74	10	CG529309	CG529309 OST109611	CG529309 OST109611
C 24	12.4	62.0	70	10	CL656659	PR10127a	CL656659 PR10127a
C 25	12.4	62.0	72	9	AZ922984	SLC05A01	AZ922984 SLC05A01
C 26	12.4	62.0	72	9	AZ922992	SLC05C05	AZ922992 SLC05C05
C 27	12.4	62.0	78	10	CM233655	104_687.1	CM233655 104_687.1
C 28	12.4	62.0	80	10	CL528379	ASV12E06	CL528379 ASV12E06
C 29	12.2	61.0	41	9	BH911786	SAIK_0721	BH911786 SAIK_0721
C 30	12.2	61.0	42	10	AL952980	Arabidops	AL952980 Arabidops
C 31	12.2	61.0	44	9	CG194788	PS110296-	CG194788 PS110296-
C 32	12.2	61.0	47	9	BZ357819	SAIK_1312	BZ357819 SAIK_1312
C 33	12.2	61.0	49	9	BZ357809	SAIK_1312	BZ357809 SAIK_1312
C 34	12.2	61.0	50	9	AZ580938	IM0369A14	AZ580938 IM0369A14
C 35	12.2	61.0	55	9	BH812903	SAIK_0634	BH812903 SAIK_0634
C 36	12.2	61.0	62	1	AA658172	nu16d02.s	AA658172 nu16d02.s
C 37	12.2	61.0	62	6	CD959074	SC7_27 Ge	CD959074 SC7_27 Ge
C 38	12.2	61.0	67	6	CD967617	SFM_213 G	CD967617 SFM_213 G
C 39	12.2	61.0	70	1	AA614030	nc82b11.s	AA614030 nc82b11.s
C 40	12.2	61.0	71	7	CK111273	Q018A05	CK111273 Q018A05
C 41	12.2	61.0	71	10	CG18238	1119052B0	CG18238 1119052B0
C 42	12.2	61.0	72	1	AA702139	z185h01.s	AA702139 z185h01.s
C 43	12.2	61.0	72	1	AU256567	AU256567	AU256567 AU256567
C 44	12.2	61.0	72	8	W89090	zh70h06.r1	W89090 zh70h06.r1
C 45	12.2	61.0	75	7	CN751990	APHL3SD-X	CN751990 APHL3SD-X
C 46	12.2	61.0	76	10	CZ481554	e03803-5P	CZ481554 e03803-5P
C 47	12.2	61.0	77	11	TA108F06P	TA108F06P	TA108F06P TA108F06P
C 48	12.2	61.0	79	9	BH903484	SAIK_1027	BH903484 SAIK_1027
C 49	12.2	61.0	80	9	CG936192	lem1080.1	CG936192 lem1080.1
C 50	12.2	61.0	24	9	AZ657045	IM0532P23	AZ657045 IM0532P23
C 51	12.2	60.0	40	10	CZ487561	E04973-5P	CZ487561 E04973-5P
C 52	12.2	60.0	41	11	TA40D01Q	TA40D01Q	TA40D01Q TA40D01Q
C 53	12.2	60.0	48	9	AZ760557	IM0554G19	AZ760557 IM0554G19
C 54	12.2	60.0	48	9	AZ772291	IM0583106	AZ772291 IM0583106
C 55	12.2	60.0	54	11	DE013515	Branchios	DE013515 Branchios
C 56	12.2	60.0	55	9	AZ634507	IM0490A24	AZ634507 IM0490A24
C 57	12.2	60.0	56	9	AZ482047	IM0306E21	AZ482047 IM0306E21
C 58	12.2	60.0	58	11	CR358826	Arabidops	CR358826 Arabidops
C 59	12.2	60.0	60	6	CF329394	NAC1--04-	CF329394 NAC1--04-
C 60	12.2	60.0	62	9	BH855545	SAIK_0849	BH855545 SAIK_0849
C 61	12.2	60.0	64	2	BE636393	SMOVAACAQ	BE636393 SMOVAACAQ
C 62	12.2	60.0	68	1	AJ654507	AJ654507	AJ654507 AJ654507
C 63	12.2	60.0	68	1	AU260014	AU260014	AU260014 AU260014
C 64	12.2	60.0	69	1	AA923001	OK76D07.s	AA923001 OK76D07.s
C 65	12.2	60.0	69	9	AZ625974	IM0465N24	AZ625974 IM0465N24
C 66	12.2	60.0	70	10	CNS02PYA	AI931422	CNS02PYA AI931422
C 67	12.2	60.0	73	1	DN856672	naa04e08	DN856672 naa04e08
C 68	12.2	60.0	74	8	DN856672	naa04e08	DN856672 naa04e08
C 69	12.2	60.0	74	9	CC455682	SAIK_0855	CC455682 SAIK_0855
C 70	12.2	60.0	75	1	AU009040	AU009040	AU009040 AU009040
C 71	12.2	60.0	75	2	BG153162	nah26G11	BG153162 nah26G11
C 72	12.2	60.0	78	1	AA884128	am31a06.s	AA884128 am31a06.s
C 73	12.2	60.0	78	7	CR415961	CR415961	CR415961 CR415961
C 74	12.2	60.0	78	9	BH810296	SAIK_0488	BH810296 SAIK_0488
C 75	12.2	60.0	78	10	CM183169	104_599-1	CM183169 104_599-1
C 76	12.2	60.0	78	10	BM92876	Arabidops	BM92876 Arabidops
C 77	12.2	60.0	79	1	AU281970	AU281970	AU281970 AU281970
C 78	12.2	60.0	79	9	CC797455	SAIK_1449	CC797455 SAIK_1449
C 79	12.2	60.0	80	9	AZ332298	IM0060A16	AZ332298 IM0060A16
C 80	12.2	60.0	80	1	AA590433	vm20D06.r	AA590433 vm20D06.r
C 81	11.8	59.0	43	10	CL528685	ASV2D02.F	CL528685 ASV2D02.F
C 82	11.8	59.0	44	9	AZ646724	IM0243G16	AZ646724 IM0243G16
C 83	11.8	59.0	51	9	AZ646724	IM0243G16	AZ646724 IM0243G16
C 84	11.8	59.0	64	11	CR131031	Forward s	CR131031 Forward s
C 85	11.8	59.0	70	1	AA707408	2127h06.s	AA707408 2127h06.s
C 86	11.8	59.0	71	8	DR082626	PMU01-020	DR082626 PMU01-020
C 87	11.8	59.0	74	10	AU596062	Arabidops	AU596062 Arabidops
C 88	11.8	59.0	78	11	CR403050	Arabidops	CR403050 Arabidops
C 89	11.8	59.0	79	1	AA046277	zk77C02.r	AA046277 zk77C02.r
C 90	11.8	59.0	79	1	AI185057	ge46604.x	AI185057 ge46604.x
C 91	11.8	59.0	80	5	BM589753	BM589753	BM589753 BM589753
C 92	11.6	58.0	30	3	BP916365	BP916365	BP916365 BP916365
C 93	11.6	58.0	37	8	W97163	mf90f05.r1	W97163 mf90f05.r1
C 94	11.6	58.0	39	10	BK650160	Arabidops	BK650160 Arabidops
C 95	11.6	58.0	40	1	AI496779	fb61c01.y	AI496779 fb61c01.y

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Matches 15; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
Qy 1 TTATGGAATGATACCGTCAT 20
   |||||:|||||
Db 25 TTCTGGATGAACAGTGAT 6

RESULT 29
AB203124
ID AB203124 standard; DNA; 50 BP.
XX
AC AB203124;
XX
DT 09-JAN-2003 (first entry)
XX
DE Human leukocyte gene expression profiling probe SEQ ID NO 3115.
XX
KW T7; leukocyte; gene expression profiling; allograft rejection;
KW atherosclerosis; congestive heart failure; systemic lupus erythematosus;
KW rheumatoid arthritis; osteoarthritis; cytomegalovirus; infection; probe;
XX
OS Homo sapiens.
XX
PN WO200257414-A2.
XX
PD 25-JUL-2002.
XX
PF 22-OCT-2001; 2001WO-US047856.
XX
PR 20-OCT-2000; 2000US-0241994P.
XX
PR 08-JUN-2001; 2001US-0296764P.
XX
PA (BIOC-) BIOCARDIA INC.
XX
PI Wohlgemuth J, Fry K, Matcuk G, Altman P, Prentice J, Phillips J;
PI Ly N, Woodward R, Queternous T, Johnson F;
XX
DR WPI; 2002-636525/68.
XX
PT New system for leukocyte expression profiling, diagnosing a disease, or
PT monitoring (the rate of) progression of a disease, e.g. atherosclerosis
PT or congestive heart failure, comprises diagnostic oligonucleotides.
XX
PS Claim 1; Page 427; Opp; English.
XX
CC The invention relates to a system for detecting gene expression, which
CC comprises one or two isolated DNA molecules that detect expression of a
CC gene, where the gene corresponds to any of 8143 oligonucleotides
CC (AB200010-AB208152) each having 50 base pairs (bp). The system is useful
CC for leukocyte expression profiling. It is particularly useful for
CC diagnosing a disease, monitoring (rate of) progression of a disease,
CC predicting therapeutic outcome, determining prognosis for a patient,
CC predicting disease complications in an individual or monitoring response
CC to treatment in an individual. The diseases include cardiac allograft
CC rejection, kidney allograft rejection, liver allograft rejection,
CC atherosclerosis, congestive heart failure, systemic lupus erythematosus,
CC rheumatoid arthritis, osteoarthritis or cytomegalovirus infection
XX
SQ Sequence 50 BP; 17 A; 13 C; 5 G; 15 T; 0 U; 0 Other;
Query Match 66.0%; Score 13.2; DB 6; Length 50;
Best Local Similarity 83.3%; Pred. No. 6.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 2 TATGGAATGATACCGTCA 19
   |||||:|||||
Db 13 TTTGGAATGATACCGACA 30

RESULT 30
AB207386
ID AB207386 standard; DNA; 50 BP.
```

```
XX
AC AB207386;
XX
DT 09-JAN-2003 (first entry)
XX
DE Human leukocyte gene expression profiling probe SEQ ID NO 7377.
XX
KW T7; leukocyte; gene expression profiling; allograft rejection;
KW atherosclerosis; congestive heart failure; systemic lupus erythematosus;
KW rheumatoid arthritis; osteoarthritis; cytomegalovirus; infection; probe;
XX
OS Homo sapiens.
XX
PN WO200257414-A2.
XX
PD 25-JUL-2002.
XX
PF 22-OCT-2001; 2001WO-US047856.
XX
PR 20-OCT-2000; 2000US-0241994P.
XX
PR 08-JUN-2001; 2001US-0296764P.
XX
PA (BIOC-) BIOCARDIA INC.
XX
PI Wohlgemuth J, Fry K, Matcuk G, Altman P, Prentice J, Phillips J;
PI Ly N, Woodward R, Queternous T, Johnson F;
XX
DR WPI; 2002-636525/68.
XX
PT New system for leukocyte expression profiling, diagnosing a disease, or
PT monitoring (the rate of) progression of a disease, e.g. atherosclerosis
PT or congestive heart failure, comprises diagnostic oligonucleotides.
XX
PS Claim 1; Page 565; Opp; English.
XX
CC The invention relates to a system for detecting gene expression, which
CC comprises one or two isolated DNA molecules that detect expression of a
CC gene, where the gene corresponds to any of 8143 oligonucleotides
CC (AB200010-AB208152) each having 50 base pairs (bp). The system is useful
CC for leukocyte expression profiling. It is particularly useful for
CC diagnosing a disease, monitoring (rate of) progression of a disease,
CC predicting therapeutic outcome, determining prognosis for a patient,
CC predicting disease complications in an individual or monitoring response
CC to treatment in an individual. The diseases include cardiac allograft
CC rejection, kidney allograft rejection, liver allograft rejection,
CC atherosclerosis, congestive heart failure, systemic lupus erythematosus,
CC rheumatoid arthritis, osteoarthritis or cytomegalovirus infection
XX
SQ Sequence 50 BP; 9 A; 17 C; 8 G; 16 T; 0 U; 0 Other;
Query Match 66.0%; Score 13.2; DB 6; Length 50;
Best Local Similarity 83.3%; Pred. No. 6.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 2 TATGGAATGATACCGTCA 19
   |||||:|||||
Db 7 TATGGAATGATACCGACA 24

Search completed: March 1, 2006, 22:51:50
Job time : 342.667 secs
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CC nucleic acid probes and detecting the hybridisation. The nucleic acid
CC probes are attached to a solid support. The analysis comprises monitoring
CC gene expression levels, identifying biallelic markers or polymorphisms,
CC or family members of a gene and a cross-species comparison. Each of the
CC nucleic acids further comprises a tag sequence. The array of nucleic acid
CC probes is useful in situ hybridisation, in Southern, Northern or dot-
CC blot hybridisation to identify or detect the sequence or specific
CC mutations of any gene, in mapping the 5' termini of mRNA molecules by
CC primer extensions or in screening cDNA or genomic libraries or subclones
CC for additional subclones containing segments of DNA that have been
CC isolated and previously sequenced. The sequence presented is one of the
CC nucleic acid probes incorporated in the microarray. Note: The sequence
CC data for this patent can also be obtained in electronic format directly
CC from USPTO at seqdata.uspto.gov/sequence.html
XX
XX
SQ Sequence 25 BP; 6 A; 4 C; 7 G; 8 T; 0 U; 0 Other;
Query Match 66.0%; Score 13.2; DB 9; Length 25;
Best Local Similarity 83.3%; Pred. No. 5.7e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
OY 1 TTATGATGATACCGTC 18
2 TTATGATGATGATACCGTC 19
Db
RESULT 27
ADX98978
ID ADX98978 standard; DNA; 30 BP.
XX
XX ADX98978;
XX
XX 05-MAY-2005 (first entry)
XX
XX PCR primer 363 used to amplify human ICAM region SNP DNA.
XX
XX SNP detection; breast tumor; endocrine disease;
XX gynecology and obstetrics; neoplasm; cytostatic; metastasis;
XX gene therapy; RNA interference; intercellular adhesion molecule; ICAM1;
XX ICAM4; ICAM5; ss; PCR; primer.
XX
XX Homo sapiens.
XX
XX MO205014846-A2.
XX
XX 17-FEB-2005.
XX
XX 27-MAY-2004; 2004WO-US016939.
XX
XX 24-JUL-2003; 2003US-0490234P.
XX 25-NOV-2003; 2003US-00723681.
XX 25-NOV-2003; 2003US-0525239P.
XX
XX (SEQU-) SEQUENOM INC.
XX
XX Roch RB, Nelson MR, Braun A, Kammerer SM, Reneland R;
XX Hoyal-Wrightson CR;
XX
XX WPI; 2005-163257/17.
XX
XX Identifying risk of, preventing and/or treating breast cancer by
XX identifying and/or analyzing polymorphic variations in nucleotide
XX sequences within the human genome.
XX
XX Example 4; Page 104; 617pp; English.
XX
XX The invention relates to a novel method for identifying a subject at risk
XX of breast cancer comprising detecting the presence or absence of a
XX polymorphic variation associated with breast cancer. The method of the
XX invention demonstrates cytostatic activity and may be useful for
XX identifying a risk of, preventing and/or treating breast cancer and
XX cancer metastasis. The methods may be utilized for gene therapy or RNA
XX interference. The current sequence is that of a PCR primer of the

CC invention which was used to amplify a human intercellular adhesion
CC molecule (ICAM1, ICAM4, ICAM5) region DNA containing a single nucleotide
CC polymorphism (SNP).
XX
XX SQ Sequence 30 BP; 9 A; 6 C; 9 G; 6 T; 0 U; 0 Other;
Query Match 66.0%; Score 13.2; DB 14; Length 30;
Best Local Similarity 83.3%; Pred. No. 5.9e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
OY 3 ATGAATGATACCGTCAT 20
8 ATGAATGATACCGTCAT 25
Db
RESULT 28
AA06134/c
ID AA06134 standard; DNA; 31 BP.
XX
XX AA06134;
XX
XX 31-MAR-1999 (first entry)
XX
XX Human biallelic polymorphic DNA fragment WI-17066.
XX
XX Polymorphism; biallelic; paternity testing; forensic; genetic mapping;
XX phenotypic typing; medicament; disease; marker; human; ss.
XX
XX Homo sapiens.
XX
XX MO9858529-A2.
XX
XX 30-DEC-1998.
XX
XX 22-JUN-1998; 98WO-US012930.
XX
XX 24-JUN-1997; 97US-0050594P.
XX
XX (AEFY-) AEFYMETRIX INC.
XX
XX Lipschutz RJ, Chee M, Fan J, Berno A;
XX
XX WPI; 1999-080963/07.
XX
XX New nucleic acid segments containing polymorphic sites - used for, e.g.
XX detecting a disease phenotype, in forensics, paternity testing or genetic
XX mapping of phenotypic traits.
XX
XX Claim 1; Page 10; 61pp; English.
XX
XX Sequences AA06101-X06558 represent human DNA fragments which contain
XX biallelic polymorphic markers. The base occupying the polymorphic site is
XX indicated by the appropriate IUPAC-IUB ambiguity code. These fragments
XX can be used in a method for determining polymorphic forms in an
XX individual. The invention further provides computer-readable storage
XX medium for storing data for access by an application programme being
XX executed on a data processing system. Such a method comprises a data
XX structure stored in the computer-readable storage medium, the data
XX structure including information resident in a database used by the
XX application programme and including records, each record comprising
XX information identifying a polymorphism shown in the above sequences. The
XX products and methods can be used for analysing polymorphic sites in
XX individuals for testing for the presence of a disease phenotype or in
XX forensics, paternity testing or genetic mapping of phenotypic traits.
XX They can also be used for the production of polypeptides expressed by
XX CC variant genes and for the production of transgenic animals. The nucleic
XX acid segments can also be used in the manufacture of medicaments for the
XX treatment or prophylaxis of diseases
XX
XX SQ Sequence 31 BP; 9 A; 8 C; 2 G; 11 T; 0 U; 1 Other;
Query Match 66.0%; Score 13.2; DB 2; Length 31;
Best Local Similarity 75.0%; Pred. No. 5.9e+03;

ID AA231919 standard; DNA; 24 BP.
 XX
 AC AA231919;
 XX
 DT 25-JAN-2000 (first entry)
 XX
 DE PCR primer for human helicase, RecQ5, coding sequence.
 XX
 KW Helicase; RecQ5; human; homeostasis; cell aging; diagnosis; PCR primer;
 KM ss.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN J011276173-A.
 XX
 PD 12-OCT-1999.
 XX
 PF 27-MAR-1998; 98BP-00081492.
 XX
 PR 27-MAR-1998; 98BP-00081492.
 XX
 PA (EIJ-1) EIJIN KENKYUSHO KK.
 XX
 DR WPI; 1999-626937/54.
 XX
 PT A gene coding helicase, RecQ5 - useful in research for elucidating the
 XX relationship to the maintenance of human homeostasis and cell aging.
 XX
 PS Example 1; Page 19; 25pp; Japanese.
 XX
 CC This sequence represents a PCR primer for DNA encoding the human helicase
 CC of the invention, designated RecQ5. The helicase RecQ5 gene can be used
 CC in a method for the diagnosis of diseases caused by an abnormality in the
 CC helicase gene. The gene can be used in researching the relationship
 CC between the maintenance of human homeostasis and cell aging
 XX
 SQ Sequence 24 BP; 5 A; 6 C; 6 G; 7 T; 0 U; 0 Other;
 XX
 QY Query Match 66.0%; Score 13.2; DB 2; Length 24;
 XX Best Local Similarity 83.3%; Pred. No. 5.7e+03;
 Db Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 1 TTATGGATGATACCGTC 18
 5 TCATGGATGATCCTGTC 22
 RESULT 25
 AAF87647
 ID AAF87647 standard; DNA; 24 BP.
 XX
 AC AAF87647;
 XX
 DT 16-JUL-2001 (first entry)
 XX
 DE Human RecQ5 alpha DNA helicase PCR primer 6F.
 XX
 KM Human; RecQ5 alpha; RecQ5 beta; RecQ5 gamma; DNA helicase;
 KW alternative splicing; chromosomal instability; PCR primer; ss.
 XX
 OS Homo sapiens.
 OS
 PN WO200125425-A1.
 XX
 PD 12-APR-2001.
 XX
 PF 25-AUG-2000; 2000WO-JP005757.
 XX
 PR 05-OCT-1999; 99JP-00284001.
 XX
 PA (AGEN-) AGENE RES INST CO LTD.
 XX

PI Furuchi Y, Shimamoto A, Kitao S, Nishikawa K;
 XX
 DR WPI; 2001-273577/28.
 XX
 PT Polynucleotide encoding for RecQ5beta helicase useful for diagnosis and
 XX treatment of chromosomal instability.
 XX
 PS Example 1; Page 29; 97pp; Japanese.
 XX
 CC The present sequence is a primer used to isolate a polynucleotide
 CC encoding a human RecQ5 type DNA helicase. The three RecQ5 type helicases
 CC alpha, beta and gamma are formed by alternative splicing. The invention
 CC discloses the RecQ5 type DNA helicases beta and gamma, and the genes
 CC encoding them. The RecQ5 beta DNA helicase has a novel characteristic of
 CC being localised in the nucleus. It is useful as a diagnostic marker or in
 CC the treatment of diseases associated with chromosomal instability
 XX
 SQ Sequence 24 BP; 5 A; 6 C; 6 G; 7 T; 0 U; 0 Other;
 XX
 QY Query Match 66.0%; Score 13.2; DB 4; Length 24;
 XX Best Local Similarity 83.3%; Pred. No. 5.7e+03;
 Db Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 1 TTATGGATGATACCGTC 18
 5 TCATGGATGATCCTGTC 22
 RESULT 26
 AC125999
 ID AC125999 standard; DNA; 25 BP.
 XX
 AC AC125999;
 XX
 DT 13-OCT-2003 (first entry)
 XX
 DE Human microarray DNA oligonucleotide SEQ ID NO 25990.
 XX
 KM EST; ss; probe; expressed sequence tag; microarray; gene expression;
 KW genetic variation; biallelic marker; polymorphism; human;
 XX cross-species comparison.
 XX
 OS Homo sapiens.
 OS
 PN US2003104410-A1.
 XX
 PD 05-JUN-2003.
 XX
 PF 15-MAR-2002; 2002US-00098263.
 XX
 PR 16-MAR-2001; 2001US-0276759P.
 XX
 PA (AFFY-) AFFYMETRIX INC.
 XX
 PI Miltmann MP;
 XX
 DR WPI; 2003-567953/53.
 XX
 PT New array of nucleic acid probes, useful for in situ hybridization, in
 PT Southern, Northern and dot-blot hybridization to identify or detect the
 PT sequence or specific mutations of any gene.
 XX
 PS Claim 1; SEQ ID NO 25990; 9pp; English.
 XX
 CC The invention discloses a microarray comprising a plurality of nucleic
 CC acid probes including one of 2,018,500 fully defined sequences, or its
 CC perfect match, perfect mismatch, antisense match or antisense mismatch.
 CC Also disclosed is a method of gene expression analysis. The array is used
 CC in monitoring gene expression levels by hybridisation to a DNA library,
 CC in analysis of genetic variation or in hybridisation of tag-labelled
 CC compounds. The nucleic acid probes are specifically designed for analysis
 CC of at least one target sequence. The method of analysis comprises
 CC hybridising at least one or more nucleic acids to at least two or more

XX The invention relates to an array for determining the chemosensitivity of
CC a cancer cell to a particular agent comprising a population of
CC polynucleotide probes designed to be complementary to and hybridize under
CC stringent conditions with a target region of at least one gene listed in
CC the specification, where at least one of the polynucleotide probes is a
CC control probe. Also included are detecting a chemosensitivity gene
CC expression profile of a cancer cell, predicting the effect of a cytotoxic
CC agent on a cancer cell obtained from a mammalian subject and
CC identifying/characterizing an agent that modulates the expression or
CC activity of one or more chemosensitivity genes. The array and methods are
CC useful for identifying the chemosensitivity gene profile of a cancer cell
CC or for determining the chemosensitivity of cells to cytotoxic agents.
CC These may also be used for identifying and characterizing new agents that
CC modulate the chemosensitivity of cancers. The present sequence is a
CC control probe used in the microarray of the invention, an RGS (not
CC defined) control.
SQ Sequence 70 BP; 23 A; 13 C; 14 G; 20 T; 0 U; 0 Other;
Query Match 68.0%; Score 13.6; DB 14; Length 70;
Best Local Similarity 80.0%; Pred. No. 4e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 TTATGAAATGATACCGTCAT 20
DB 2 TTATGAAATGATCCTGGAAAT 21
RESULT 22
AD217963
ID AD217963 standard; DNA; 21 BP.
XX AD217963;
XX 16-JUN-2005 (first entry)
DE Beverage-spoiling microorganism detection-related oligo probe SeqID270.
XX food; microorganism detection; microorganism identification; water;
KM waste-water; probe; ss; DNA detection.
XX Leuconostoc.
OS
XX WO2005031004-A2.
PN
XX 07-APR-2005.
PD
XX 23-SEP-2004; 2004WO-EP010695.
PF
XX 23-SEP-2003; 2003DE-01044057.
PR
XX (VERM-) VERMICON AG.
PA
XX Snaird J, Beimfohr C, Thelen K, Lehner A;
PI WPI; 2005-273397/28.
DR
XX Detecting spoilage microorganisms in beverages, particularly non-
PT alcoholic, by hybridization testing with specific oligonucleotides.
XX
XX Claim 1; SEQ ID NO 270; 328bp; German.
PS
XX This invention relates to a novel method for detecting beverage-spoiling
CC microorganisms using at least one of 1138 oligonucleotide probes fully
CC defined in the specification. The method is especially used to detect
CC beverage-spoiling microorganisms in alcohol-free beverages, for example
CC fruit-based drinks or water, but may also be extended to analysis of
CC soil, plant parts, waste water, silage, clinical samples (feces, blood or
CC tissues), foods, cosmetics and pharmaceuticals. The method provides rapid
CC (1-2 days, compared to up to 10 days for classical culture methods) and
CC specific detection of spoilage microorganisms. It combines the advantages
CC of classical fluorescent in situ hybridization with those of culture

CC methods, can differentiate between closely related organisms, is suitable
CC for screening large numbers of samples and allows simultaneous detection
CC of several different microorganisms. The present sequence is that of an
CC oligonucleotide probe which may be used for detecting Beverage-spoiling
CC microorganisms in the method of the invention.
SQ Sequence 21 BP; 2 A; 6 C; 5 G; 8 T; 0 U; 0 Other;
Query Match 66.0%; Score 13.2; DB 14; Length 21;
Best Local Similarity 83.3%; Pred. No. 5.6e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 TTATGAAATGATACCGTC 18
DB 4 TTCTGAAATGATACCGTC 21
RESULT 23
AA21679
ID AA21679 standard; DNA; 24 BP.
XX AA21679;
AC
XX 14-MAY-1999 (first entry)
DT
XX Human helicase gene RecQ4 primer.
DE
XX RecQ4 gene; helicase; Werner's syndrome; Bloom's syndrome; human;
KW PCR primer; ss.
XX
XX Synthetic.
OS
XX Homo sapiens.
XX
XX WO9905284-A1.
PN
XX 04-FEB-1999.
PD
XX 10-JUL-1998; 98WO-JP003114.
PF
XX 25-JUL-1997; 97JP-00200387.
PR
XX (AGEN-) AGENE RES INST CO LTD.
PA
XX Shimamoto A, Kitao S, Furuchi Y;
PI WPI; 1999-142939/12.
DR
XX New human helicase gene RecQ4 - used for investigation and diagnosis of
PT helicase-implicated diseases such as Werner's syndrome.
XX
XX Disclosure; Page 55; 67pp; Japanese.
XX
XX The invention relates to a human gene RecQ4 encoding a protein having
CC helicase activity. The gene has significant homology to the Escherichia
CC coli helicase gene (RecQ). Host cells transformed with vectors comprising
CC the RecQ4 gene are used for the recombinant expression of the protein.
CC The gene may be used for the study and diagnosis of disorders in which
CC helicase activity is involved, such as Werner's and Bloom's syndromes in
CC which mutations in the helicase gene are implicated
SQ Sequence 24 BP; 5 A; 6 C; 6 G; 7 T; 0 U; 0 Other;
Query Match 66.0%; Score 13.2; DB 2; Length 24;
Best Local Similarity 83.3%; Pred. No. 5.7e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 TTATGAAATGATACCGTC 18
DB 5 TCATGAAATGATCCTGTC 22
RESULT 24
AA231919

DR WPI: 2004-043125/04.
XX Identifying nucleic acid ligand of target molecule from mixture
PT comprising single stranded nucleic acids having region of randomised
PT sequence by contacting mixture with target molecule, amplifying affinity
PT nucleic acids.
PS Claim 27; SEQ ID NO 47; 90pp; English.
XX
XX This invention relates to a novel method (CE-SELEX, Capillary
CC Electrophoresis-Systematic Evolution of ligands by Exponential
CC enrichment) of identifying nucleic acid ligands of a target molecule from
CC a candidate mixture comprised of single stranded nucleic acids each
CC having a region of randomised sequence by contacting the mixture with the
CC target molecule, where nucleic acids having affinity to the target
CC molecule are partitioned from the mixture by capillary electrophoresis,
CC amplifying increased affinity nucleic acids to yield a ligand-enriched
CC mixture of nucleic acids. The invention may be useful for the production
CC of compounds with an antiaesthetic, cerebroprotective, anti-HIV or
CC virucide activity. The method is useful for identifying nucleic acid
CC ligands of a target molecule from a candidate mixture comprised of single
CC stranded nucleic acids each having a region of randomised sequence.
CC Aptamers identified by the method are useful as a tool in analytical
CC chemistry, useful in wide range of diagnostic assays and as direct
CC benefits to many areas of the research, including biomedical and health
CC research. Improved aptamers are useful in developing diagnostic assays,
CC for example as diagnostic markers in medical analysis, in vivo imaging
CC and biosensors. The aptamers are also useful in quantitating targets
CC present in complex matrices. The aptamers are used to develop high-
CC sensitivity affinity probe capillary electrophoresis (APCE) assays, in
CC ELISA type assays using enzyme-linked DNA aptamers. Thrombin aptamers may
CC be developed for using fibre-optic microarray biosensors. Aptamers
CC against transformed endothelial cells may be selected for use as
CC histological markers to identify tumour microvessels. Aptamers may be
CC developed for use in other aptamer-based assays, such as assays for
CC analytes ranging from anthrax spores to cocaine. Aptamers having improved
CC quality, improved binding efficiency and selectivity can be identified by
CC the method of the invention. The present sequence is that of an aptamer
CC DNA sequence which was identified using the method of the invention.
XX
SQ Sequence 80 BP; 22 A; 24 C; 20 G; 14 T; 0 U; 0 Other;
Query Match 69.0%; Score 13.8; DB 12; Length 80;
Best Local Similarity 88.2%; Pred. No. 3.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 4 TGGATGATACCGTCAT 20
DB 34 TGGATCGATCCGTCAT 18
RESULT 18
AA267315
ID AA267315 standard; DNA; 47 BP.
XX
AC AA267315;
XX
DT 10-SEP-2001 (first entry)
XX
DE Human map-related biallelic marker SEQ ID NO:1662.
XX
XX Human genome; biallelic marker; high density disequilibrium map;
KW genomic map; haplotype; phenotype; polymorphic base; genotyping;
KW haplotyping; hybridization; identification; characterisation; diagnosis;
KW single nucleotide polymorphism; SNP; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT replace(24,G)
FT variation /*tag= a
FT /standard_name= "single nucleotide polymorphism"
XX

PN MO9954500-A2.
XX
XX 28-OCT-1999.
PD
XX
XX 21-APR-1999; 99MO-IB000822.
PF
XX
XX 21-APR-1998; 98US-0082614P.
PR
XX 23-NOV-1998; 98US-0109732P.
XX
XX (GEST) GENSET.
XX
XX Cohen D, Blumenfeld M, Chumakov I;
PI
XX WPI: 2000-013267/01.
DR
XX
XX Novel biallelic markers used to construct a high density disequilibrium
PT map of the human genome.
XX
XX
XX Claim 1; Page 585; 2745pp; English.
XX
XX AA265654 to AA269578 represent human biallelic markers from the present
CC invention, which contain a polymorphic base at position 24 of their
CC nucleotide sequences. AA269579 to AA277440 represent amplification
CC primers for the biallelic markers. The biallelic markers of the invention
CC have a variety of uses; they can be used for high density mapping of the
CC human genome, and in complex association studies and haplotyping studies
CC which are useful in determining the genetic basis for disease states.
CC Compositions and methods of the invention can also be useful for the
CC identification of the targets for the development of pharmaceutical
CC agents and diagnostic methods, as well as the characterisation of the
CC differential efficacious responses to and side effects from
CC pharmaceutical agents acting on a disease as well as other treatment.
CC N.B. The SEQ ID Nos 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and
CC 3367, are not actually given a sequence in the Sequence Listing from the
CC present invention
XX
SQ Sequence 47 BP; 18 A; 4 C; 10 G; 15 T; 0 U; 0 Other;
Query Match 68.0%; Score 13.6; DB 3; Length 47;
Best Local Similarity 80.0%; Pred. No. 3.8e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 TTATGATGATACCGTCAT 20
DB 27 TTATPAAAAGATTCGTCAT 46
RESULT 19
AB203677
ID AB203677 standard; DNA; 50 BP.
XX
XX AB203677;
XX
XX
DT 09-JAN-2003 (first entry)
XX
XX Human leukocyte gene expression profiling probe SEQ ID NO 3668.
DE
XX
XX T7; leukocyte; gene expression profiling; allograft rejection;
KW atherosclerosis; congestive heart failure; systemic lupus erythematosus;
KW rheumatoid arthritis; osteoarthritis; cytomegalovirus; infection; probe;
KW ds.
XX
OS Homo sapiens.
XX
XX MO200257414-A2.
PN
XX
XX 25-JUL-2002.
PD
XX
XX 22-OCT-2001; 2001WO-US047856.
PF
XX
XX 20-OCT-2000; 2000US-0241994P.
PR
XX 08-JUN-2001; 2001US-0296764P.
XX

PT New membrane scaffold protein for forming nanoscale particles, useful in
PT biological research, self assemblies with(out) phospholipids into a
PT nanoscale particle in an aqueous environment.

PS Example 2; Page 40; 112pp; English.

XX The invention relates to a membrane scaffold protein (MSP), that self
CC assembles in the absence of phospholipid, with a phospholipid or a
CC mixture of phospholipids, into a nanoscale particle of 5-500 nm in
CC diameter, in an aqueous environment, where the membrane scaffold protein
CC is amphipathic and forms at least one alpha helix. The nanoscale particle
CC comprising MSP is useful for identifying a competitor of binding of a
CC ligand to a receptor protein which is incorporated within the nanoscale
CC particle together with MSP, by contacting nanoscale particle and a
CC receptor protein with a detectable ligand to produce nanoscale particle-
CC bound detectable ligand, contacting the bound ligand with a test
CC compound, and measuring detectable ligand released from the particle,
CC such that a competitor of ligand binding is identified when contacting
CC the bound ligand results in release of the detectable ligand. The
CC invention is useful for the incorporation of additional hydrophobic or
CC partially hydrophobic protein molecules. The nanoscale particle can form
CC tags for purification and physical manipulation of disks such as in
CC hydrogels on or a gold biosensor surface, and they can serve as entitles
CC for rapid and reproducible assay and crystallisation. The nanoscale
CC particle and MSP are useful in biotechnology, pharmaceutical industries
CC and in research areas. The nanoscale particle is useful for structure/
CC function correlation, structure determination, bioseparation and drug
CC discovery. The present sequence is a synthetic oligonucleotide used to
CC construct synthetic MSP gene

XX Sequence 54 BP; 22 A; 6 C; 12 G; 14 T; 0 U; 0 Other;

Query Match 69.0%; Score 13.8; DB 6; Length 54;
Best Local Similarity 88.2%; Pred. No. 3.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 ATGGAATGATACCGTCA 19
DB 37 ATGGAATTATATCGTCA 53

RESULT 16
AAD39720/c
ID AAD39720 standard; DNA; 80 BP.

XX AAD39720;

XX 22-OCT-2002 (first entry)

DE Synthetic oligo caps3b used to construct synthetic MSP gene.

XX Membrane scaffold protein; MSP; phospholipid; nanoscale particle;
KM hydrogel; gold biosensor surface; reproducible assay; crystallisation;
KM biotechnology; pharmaceutical industry; structure determination;
KM bioseparation; drug discovery; ss.

XX Unidentified.

XX WO200240501-A2.

XX 23-MAY-2002.

XX 20-NOV-2001; 2001MO-US043451.

XX 20-NOV-2000; 2000US-0252233P.

XX (UNIT) UNIV ILLINOIS FOUND.

XX Sligar SG, Bayburt TH;

XX WPI, 2002-500201/53.

XX New membrane scaffold protein for forming nanoscale particles, useful in

PT biological research, self assemblies with(out) phospholipids into a
PT nanoscale particle in an aqueous environment.

PS Example 2; Page 41; 112pp; English.

XX The invention relates to a membrane scaffold protein (MSP), that self
CC assembles in the absence of phospholipid, with a phospholipid or a
CC mixture of phospholipids, into a nanoscale particle of 5-500 nm in
CC diameter, in an aqueous environment, where the membrane scaffold protein
CC is amphipathic and forms at least one alpha helix. The nanoscale particle
CC comprising MSP is useful for identifying a competitor of binding of a
CC ligand to a receptor protein which is incorporated within the nanoscale
CC particle together with MSP, by contacting nanoscale particle and a
CC receptor protein with a detectable ligand to produce nanoscale particle-
CC bound detectable ligand, contacting the bound ligand with a test
CC compound, and measuring detectable ligand released from the particle,
CC such that a competitor of ligand binding is identified when contacting
CC the bound ligand results in release of the detectable ligand. The
CC invention is useful for the incorporation of additional hydrophobic or
CC partially hydrophobic protein molecules. The nanoscale particle can form
CC tags for purification and physical manipulation of disks such as in
CC hydrogels on or a gold biosensor surface, and they can serve as entitles
CC for rapid and reproducible assay and crystallisation. The nanoscale
CC particle and MSP are useful in biotechnology, pharmaceutical industries
CC and in research areas. The nanoscale particle is useful for structure/
CC function correlation, structure determination, bioseparation and drug
CC discovery. The present sequence is a synthetic oligonucleotide used to
CC construct synthetic MSP gene

XX Sequence 80 BP; 13 A; 23 C; 19 G; 25 T; 0 U; 0 Other;

Query Match 69.0%; Score 13.8; DB 6; Length 80;
Best Local Similarity 88.2%; Pred. No. 3.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 ATGGAATGATACCGTCA 19
DB 80 ATGGAATTATATCGTCA 64

RESULT 17
ADM79905/c
ID ADM79905 standard; DNA; 80 BP.

XX ADM79905;

XX 03-JUN-2004 (first entry)

DE DNA ligand identification-related aptamer DNA sequence SeqID47.

XX CE-SELEX; capillary electrophoresis; ligand-enriched mixture;
KM analytical chemistry; in vivo imaging; biosensor; complex matrix;
KM affinity probe capillary electrophoresis; APCE; ELISA;
KM fibre-optic microarray biosensor; histological marker;
KM tumour microvessel; anthrax spore; cocaine; ds.

XX Unidentified.

XX Synthetic.

XX WO2003102212-A2.

XX 11-DEC-2003.

XX 29-MAY-2003; 2003WO-US016796.

XX 31-MAY-2002; 2002US-0384709P.

XX (MINU) UNIV MINNESOTA.

XX Bowser MT, Mendonsa SD;

PT Bacterial strain simultaneously expressing a fusion protein, signal
PT peptide-heterologous protein-subunit of bacterial surface structure, and
PT periplasmic chaperone specific for recombinant heterologous protein.
XX
XX Example 3; Page 27; 49pp; English.
XX
CC The invention relates to a bacterial strain, particularly an *Escherichia*
CC coli strain for the secretion of soluble, biologically active recombinant
CC heterologous proteins into the periplasm or culture medium. The bacterial
CC strain expresses a fusion protein comprising a signal peptide, a mature
CC heterologous protein, and a bacterial surface protein subunit
CC simultaneously with a periplasmic chaperone and an outer membrane protein
CC usher/secretin protein, both of which are specific for the surface
CC protein subunit component of the fusion protein. In particular, the
CC signal peptide and surface protein subunit are from the *Yersinia pestis*
CC Caf1 protein, and the periplasmic chaperone and outer membrane protein
CC usher/secretin are *Y. pestis* CafM and CafA respectively. The bacterial
CC strain of the invention is useful for producing heterologous recombinant
CC proteins such as granulocyte macrophage-colony stimulating factor (GM-
CC CSF), interleukin-1-beta (IL-1-beta), and IL-1 receptor antagonist (IL-
CC 1ra). The present sequence represents a *Yersinia pestis* CafM PCR primer
CC used in an exemplification of the invention
XX
SQ Sequence 26 BP; 5 A; 5 C; 9 G; 7 T; 0 U; 0 Other:
Query Match 71.0%; Score 14.2; DB 4; Length 26;
Best Local Similarity 84.2%; Pred. No. 1.7e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 TTATGAATGATACCGTCA 19
Db 21 TTACGAATGTATCCGACA 3
RESULT 12
ABD292294
ID ABD292294 standard; DNA; 20 BP.
XX
XX ABD292294;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.
XX
XX Human; antisense; lung dysfunction; nasal airway dysfunction;
KM antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KM antisthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KM antisense gene therapy; respiratory; lung; adenosine sensitivity;
KM adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
XX lung inflammation; respiratory disease; ds.
XX
XX Homo sapiens.
OS
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
XX (EPIG-) EPIGENESIS PHARM INC.
XX
PI Myce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
XX ublquinone.
XX

PS Disclosure, SEQ ID NO 7536; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antisthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 7 A; 4 C; 3 G; 5 T; 0 U; 1 Other:
Query Match 69.0%; Score 13.8; DB 10; Length 20;
Best Local Similarity 83.3%; Pred. No. 2.7e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 3 ATGAATGATACCGTCAT 20
Db 1 ATGAATTAACCGNCAT 18
RESULT 13
ABD28524
ID ABD28524 standard; DNA; 20 BP.
XX
XX ABD28524;
XX
DT 29-JUL-2004 (first entry)
XX
DE R14663-derived oligonucleotide SEQ ID 7536.
XX
XX Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;
KM respiratory tract inflammation; adenosine sensitivity; lung; cancer;
KM surfactant depletion; antiallergic; antiinflammatory; antisthmatic;
KM analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;
KM beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;
KM respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;
KM emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;
KM pulmonary transplantation rejection; ss; primer.
XX
XX Homo sapiens.
OS
XX
PN WO200285309-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013143.
XX
PR 24-APR-2001; 2001US-0286036P.
XX
XX (EPIG-) EPIGENESIS PHARM INC.
XX
PI Myce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-093058/08.
XX
PT Pharmaceutical composition for treating asthma, has antisense
PT oligonucleotide containing less percentage of adenosine, targeted to
PT nucleic acids associated with lung airway or lung dysfunction, and

KW co-suppression; chaumatin; sweetener; sucrose phosphate synthase;
 KM lycopene cyclase; polygalacturonase inhibiting protein; glucanase;
 XX chitinase; PCR; primer; ss.
 OS Synthetic.
 OS Rubus idaeus.
 XX WO9727308-A1.
 PN 31-JUL-1997.
 PD 27-JAN-1997; 97WO-US001443.
 PF 29-JAN-1996; 96US-00592936.
 PR (AGRI-) AGRITROPE INC.
 PA (AGRI-) AGRITROPE INC.
 XX Kellogg JA, Bestwick RK;
 PI WPI; 1997-393694/36.
 DR
 XX
 PT Plant fruit, especially raspberry, drul promoter - useful for high level,
 PT tissue specific expression of heterologous sequences, especially to
 PT modify ethylene production.
 PS Example 4; Page 33; 67pp; English.
 XX
 PS PCR primers Drugen5' (AAT86744) and Drugen3' (AAT86745) are based on a
 CC raspberry drul cDNA sequence (see AAT86743). They were used in the PCR
 CC amplification of raspberry leaf genomic DNA. A drul genomic clone (see
 CC AAT86746) was obtained. Inverse PCR (see (AAT86747-48) was then used to
 CC isolate a genomic clone (see AAT86749) that included the drul 5' flanking
 CC region. The drul promoter (see AAT86739) is used in claimed chimeric
 CC genes for the high-level, tissue-specific expression of heterologous
 CC sequences in transgenic plants, especially to modify ethylene production
 CC
 SQ Sequence 22 BP; 7 A; 4 C; 5 G; 6 T; 0 U; 0 Other;
 Query Match 71.0%; Score 14.2; DB 2; Length 22;
 Best Local Similarity 84.2%; Pred. No. 1.7e+03;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Oy 1 TTATGCAATGATACCGTCA 19
 Db 20 TTATGCACTAATACCGTCA 2
 RESULT 10
 AAT86857/c
 ID AAT86857 standard; DNA; 22 BP.
 XX
 AC AAT86857;
 XX
 DT 09-FEB-1998 (first entry)
 DT
 XX
 DE Raspberry drul gene PCR primer Drugen3'.
 XX
 KW Promoter; drul; drul10; drul259; drupel; raspberry; transgenic plant;
 KW tissue-specific gene expression; neomycin phosphotransferase;
 KW hygromycin phosphotransferase; bromoxynil-specific nitrilase;
 KW selectable marker; herbicide resistance; fruit; primer; PCR; ss.
 XX
 OS Synthetic.
 OS Rubus idaeus.
 XX WO9727307-A1.
 PN 31-JUL-1997.
 PD 28-JAN-1997; 97WO-US001275.
 PF 29-JAN-1996; 96US-00592936.
 PR 24-JAN-1997; 97US-00788928.

XX
 PA (AGRI-) AGRITROPE INC.
 XX
 PI Kellogg JA, Bestwick RK;
 XX
 DR WPI; 1997-402206/37.
 XX
 PT Raspberry promoters drul, drul10 and drul259 - used for genetic
 PT engineering of plants, e.g. to provide moderate expression of selectable
 PT marker allowing growth in presence of selective agent.
 PS Example 4; Page 56; 84pp; English.
 XX
 PS PCR primers Drugen5' (AAT86856) and Drugen3' (AAT86857) are based on a
 CC raspberry drul cDNA sequence (see AAT86855). They were used to amplify
 CC raspberry genomic DNA, yielding a partial drul clone (see AAT86858). The
 CC 5' flanking region of drul was subsequently recovered. Promoters (see
 CC AAT86849-51) based on the drul gene promoter are used in claimed chimeric
 CC genes to provide constitutive expression of heterologous sequences in
 CC transgenic plants, especially to provide selectable markers or to confer
 CC herbicide resistance
 CC
 SQ Sequence 22 BP; 7 A; 4 C; 5 G; 6 T; 0 U; 0 Other;
 Query Match 71.0%; Score 14.2; DB 2; Length 22;
 Best Local Similarity 84.2%; Pred. No. 1.7e+03;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Oy 1 TTATGCAATGATACCGTCA 19
 Db 20 TTATGCACTAATACCGTCA 2
 RESULT 11
 AAC87300/c
 ID AAC87300 standard; DNA; 26 BP.
 XX
 AC AAC87300;
 XX
 DT 09-MAR-2001 (first entry)
 DT
 XX
 DE Yersinia pestis CafIM periplasmic chaperone PCR primer #1.
 XX
 KW Bacterial expression system; periplasmic secretion; Escherichia coli;
 KW Yersinia pestis CafI; periplasmic chaperone CafIM;
 KW usher/secretin protein CafIA; IL-1-beta; interleukin-1-beta; GM-CSF;
 KW granulocyte macrophage-colony stimulating factor; IL-1ra;
 KW IL-1 receptor antagonist; fusion gene; fusion protein; junction region;
 KW PCR primer; ss.
 XX
 OS Yersinia pestis.
 OS WO200066756-A1.
 PN 09-NOV-2000.
 PD 03-MAY-2000; 2000WO-FI000387.
 PF 04-MAY-1999; 99FI-00001014.
 PR (KORP/) Korpela T.
 PA (MACI/) MACINTYRE-AYANE S.
 PA (ZAVI/) ZAVIALOV A V.
 PA (BAT/) BATCHIKOVA N V.
 PA (PETR/) PETROVSKAYA L E.
 PA (KORO/) KOROBO V G.
 PA (ZAVY/) ZAV'YALOV V P.
 XX
 PI Korpela T, Macintyre-Ayane S, Zavialov AV, Batchikova NV;
 PI Petrovskaya LE, Korobko VG, Zav'yalov VP;
 DR WPI; 2001-007229/01.

OS Pinus radiata.
 XX
 PN WO2005065339-A2.
 XX
 PD 21-JUL-2005.
 XX
 PF 30-DEC-2004; 2004WO-US043804.
 XX
 PR 30-DEC-2003; 2003US-0533036P.
 XX
 PA (ARBO-) ARBOGEN LLC.
 PA (GENE-) GENESIS RES & DEV CORP LTD.
 XX
 PI Forster RL, Connert MB, Emerson SJ, Grigor MR, Higgins CM,
 PI Lund ST, Magusin A, Kodrzycki RJ;
 XX
 DR WPI; 2005-506765/51.
 XX
 PT New polynucleotide encoding a plant cell cycle protein, useful for
 PT modifying plant development and altering plant phenotype.
 PS
 PS Claim 43; SEQ ID NO 556; 499pp; English.
 XX
 CC The invention describes an isolated polynucleotide comprising: (1) a
 CC sequence of SEQ ID NOS: 1-237 or their conservative variants; (11) a
 CC sequence encoding the catalytic or substrate-binding domain of a
 CC polypeptide of SEQ ID NOS: 261-497, where the polynucleotide encodes a
 CC polypeptide having the activity of the polypeptide of SEQ ID NOS: 261-497
 CC ; or (11i) a nucleic acid sequence of SEQ ID NOS: 471-697. Also described
 CC are: (1) a DNA construct comprising at least one polynucleotide having
 CC the sequence of SEQ ID NOS: 1-237 or their conservative variants; (2) a
 CC plant cell transformed with the DNA construct of (1); (3) a transgenic
 CC plant comprising the plant cell of (2); (4) a method of making a
 CC transformed plant; (5) a wood or a wood pulp obtained from a transgenic
 CC tree which has been transformed with the DNA construct of (1); (6) a
 CC method of making wood or wood pulp; (7) an isolated polypeptide
 CC comprising an amino acid sequence encoded by the new isolated
 CC polynucleotide or comprising any of the amino acid sequences of SEQ ID
 CC NOS: 261-497; (8) a method of altering a plant phenotype of a plant; (9)
 CC a method of correlating gene expression in two different samples; (10) a
 CC method of correlating the possession of a plant phenotype to the level of
 CC gene expression in the plant of one or more genes; (11) a method of
 CC correlating gene expression to a stage of the cell cycle; (12) a
 CC combination, for detecting expression of one or more genes, comprising
 CC two or more oligonucleotides, where each oligonucleotide is capable of
 CC hybridizing to a nucleic acid sequence of SEQ ID NOS: 1-237 or to gene
 CC product encoded by a nucleic acid sequence of SEQ ID NOS: 1-237; (13) a
 CC microarray comprising the combination of (12) provided on a solid
 CC support, where each of the two or more oligonucleotides occupies a unique
 CC location on the solid support; (14) a method for detecting one or more
 CC genes in a sample; (15) a method for detecting one or more nucleic acid
 CC sequences encoded by one or more genes in a sample; and (16) a kit, for
 CC detecting gene expression, comprising the microarray of (13) together
 CC with one or more buffers or reagents for a nucleotide hybridization
 CC reaction. The polynucleotides, polypeptides, DNA construct, composition,
 CC and methods are useful for modifying plant development and altering plant
 CC phenotype. This sequence represents an oligonucleotide used in the
 CC creation of a microarray for detection of cell cycle genes.
 XX
 SQ Sequence 60 BP; 14 A; 12 C; 13 G; 21 T; 0 U; 0 Other;
 Query Match 84.0%; Score 16.8; DB 14; Length 60;
 Best Local Similarity 90.0%; Pred. No. 80;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 TTATGGAATGATACCGTCAT 20
 |||||
 DB 44 TTATGGAAGATACGTCAT 25
 |||||
 RESULT 8
 ADT55403/c
 ID ADT55403 standard; DNA; 20 BP.

XX ADT55403;
 AC
 XX 30-DEC-2004 (first entry)
 DT
 XX
 DE Human HDAC3 isoform, HDAC3sv1.2 specific probe.
 XX
 XX HDAC3; histone deacetylase 3; immune response; transcription modulator;
 XX human; probe; ss.
 OS Homo sapiens.
 XX
 PN US2004197888-A1.
 XX
 PD 07-OCT-2004.
 XX
 PF 22-DEC-2003; 2003US-00745242.
 XX
 PR 31-DEC-2002; 2002US-0437666P.
 PR 12-JUN-2003; 2003US-0478233P.
 XX
 PA (ARMO/) ARMOUR C D.
 PA (LOER/) LOERCH P M.
 PA (CAST/) CASTLE J C.
 PA (JOHN/) JOHNSON J M.
 XX
 PI Armour CD, Loerch PM, Castle JC, Johnson JM;
 XX
 DR WPI; 2004-709096/69.
 XX
 CC New human histone deacetylase 3 nucleic acid, useful as hybridization
 CC probes or PCR primer for identifying nucleic acids encoding for proteins
 CC related to histone deacetylase, or for the recombinant expression of
 CC histone deacetylase.
 XX
 PS disclosure; SEQ ID NO 31; 37pp; English.
 XX
 CC The present invention relates to a nucleic acids and polypeptides
 CC encoding four novel splice variant isoforms of human histone deacetylase
 CC 3 (HDAC3). The human HDAC3 nucleic acid is useful as hybridization probes
 CC or PCR primer for identifying nucleic acids encoding for proteins related
 CC to histone deacetylase, or for the recombinant expression of histone
 CC deacetylase. The HDAC3 polypeptides are useful for enhancing an immune
 CC response and modulating transcription activity or levels of histone
 CC deacetylation. The present sequence is the human HDAC3 isoform,
 CC HDAC3sv1.2 specific probe.
 XX
 SQ Sequence 20 BP; 5 A; 6 C; 4 G; 5 T; 0 U; 0 Other;
 Query Match 76.0%; Score 15.2; DB 13; Length 20;
 Best Local Similarity 85.0%; Pred. No. 4.9e+02;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 TTATGGAATGATACCGTCAT 20
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 DB 20 TTGTGGAAGACACCGTCAT 1
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 RESULT 9
 AAT86745/c
 ID AAT86745 standard; DNA; 22 BP.
 XX
 AC AAT86745;
 XX
 DT 05-FEB-1998 (first entry)
 XX
 DE PCR primer DrugEn3' used for drul genomic DNA amplification.
 XX
 KW Promoter; drul; raspberry; transgenic plant; fruit; ripening;
 KW tissue-specific gene expression; ethylene;
 KW S-adenosylmethionine hydrolase;
 KW aminocyclopropane-1-carboxylic acid deaminase; ACC deaminase;
 KW aminocyclopropane-1-carboxylic acid oxidase; ACC oxidase; antisense;

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OS Synthetic.
XX Key Location/Qualifiers
FH modified_base 1..20
FT /tag= b
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone where all cytidines are
FT 5-methyl cytidines"
FT modified_base 1..5
FT /tag= a
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"
FT modified_base 16..20
FT /tag= c
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"
XX US2003236204-A1.
XX 25-DEC-2003.
XX 14-JUN-2002; 2002US-00173192.
XX 14-JUN-2002; 2002US-00173192.
XX (ISIS-) ISIS PHARM INC.
XX Monia BP, Dobie KW;
XX WPI; 2004-070606/07.
XX New antisense oligonucleotide compound, useful for diagnosing, preventing
XX and/or treating conditions with aberrant activity of the histone
XX deacetylase 2, such as cancer, inflammation and metabolic disorders.
XX Example 15; SEQ ID NO 34; 46bp; English.
XX PS The present invention relates to antisense compounds, compositions and
XX CC methods used for modulating histone deacetylase 2 (HDAC2). The methods
XX CC and compositions of the present invention are useful for the diagnosis,
XX CC prevention and/or treatment of diseases or conditions associated with
XX CC aberrant expression or activity of histone deacetylase 2, such as a
XX CC hyperproliferative disorder (cancer), a condition involving an
XX CC inflammatory response or an aberrant apoptosis and a metabolic disorder.
XX CC The invention is also useful in antisense-therapy. The present sequence
XX CC is human histone deacetylase 2 DNA antisense oligonucleotide used in the
XX CC exemplification of the invention.
XX SQ Sequence 20 BP; 6 A; 3 C; 4 G; 7 T; 0 U; 0 Other;
XX
XX Query Match 95.0%; Score 19; DB 12; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 4.7;
XX Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 2 TATGAATGATACCGTCAT 20
XX ||||||||||||||||
XX DB 1 TATGAATGATACCGTCAT 19
XX
XX RESULT 6
XX ADN49063
XX ID ADN49063 standard; DNA; 20 BP.
XX AC ADN49063;
XX
XX 15-JUN-2004 (first entry)
XX
XX Human HDAC2 specific antisense oligo, ISIS 157265.
XX
XX Histone deacetylase 2; HDAC2; HDAC2; hda2; RPD3; hRPD3;
XX hyperproliferative disorder; cancer; antisense gene therapy; human;
XX antisense; phosphorothioate backbone; ss.
XX
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OS Homo sapiens.
OS Synthetic.
XX Key Location/Qualifiers
FH modified_base 1..20
FT /tag= b
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone in which all cytidines
FT are 5-methylcytidines"
FT modified_base 1..5
FT /tag= a
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl bases"
FT modified_base 16..20
FT /tag= c
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl bases"
XX US2004077578-A1.
XX 22-APR-2004.
XX 02-SEP-2003; 2003US-00653528.
XX 14-JUN-2002; 2002US-00173192.
XX (MONI/) MONIA B P.
XX (DOBI/) DOBIE K W.
XX Monia BP, Dobie KW;
XX WPI; 2004-340037/31.
XX New compound, having a sequence targeted to a coding region of a nucleic
XX acid encoding human histone deacetylase 2, useful for preparing a
XX composition for treating hyperproliferative disorders, e.g., cancer.
XX Example 15; SEQ ID NO 34; 47bp; English.
XX PS The invention relates to antisense compounds, compositions and methods
XX CC for modulating the expression of histone deacetylase 2 (HDAC2). HDAC2 is
XX CC also known as HDAC-2, hda2, human RPD3 and hRPD3. The composition
XX CC comprises antisense compounds that can be targeted towards HDAC2. The
XX CC compound is useful for preparing a composition for treating
XX CC hyperproliferative disorders, e.g., cancer. It is also useful in
XX CC antisense gene therapy. The present sequence is an antisense
XX CC oligonucleotide targeted to human HDAC2 DNA.
XX SQ Sequence 20 BP; 6 A; 3 C; 4 G; 7 T; 0 U; 0 Other;
XX
XX Query Match 95.0%; Score 19; DB 12; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 4.7;
XX Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 2 TATGAATGATACCGTCAT 20
XX ||||||||||||||||
XX DB 1 TATGAATGATACCGTCAT 19
XX
XX RESULT 7
XX AEB27395/C
XX ID AEB27395 standard; DNA; 60 BP.
XX AC AEB27395;
XX
XX 22-SEP-2005 (first entry)
XX
XX P. radiata cell cycle gene microarray oligo SEQ ID NO 556.
XX
XX plant protectant; fungicide; plant growth regulant; gene therapy;
XX cell cycle; gene expression; plant; transgenic plant; microarray; wood;
XX ss.
XX
```

```
RESULT 3
ADN49062
ID ADN49062 standard; DNA; 20 BP.
XX
AC ADN49062;
XX
DT 15-JUL-2004 (first entry)
XX
DE Human HDAC2 specific antisense oligo, ISIS 157264.
XX
KM Histone deacetylase 2; HDAC2; HDAC2; hda2; RPD3; hRPD3;
KW hyperproliferative disorder; cancer; antisense gene therapy; human;
KW anticancer; phosphorothioate backbone; ss.
XX
OS Homo sapiens.
XX
XX Synthetic.
XX
FH Key
FT modified_base 1..20 Location/Qualifiers
FT FT /tag= b
FT FT /mod_base= OTHER
FT FT /note= "Phosphorothioate backbone in which all cytidines
FT FT are 5-methylcytidines"
FT FT 1..5
FT FT /tag= a
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FT FT /note= "2'-methoxyethyl bases"
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FT FT /note= "2'-methoxyethyl bases"

US2004077578-A1.
XX
PD 22-APR-2004.
XX
PF 02-SEP-2003; 2003US-00653528.
XX
PR 14-JUN-2002; 2002US-00173192.
XX
PA (MONI/) MONIA B P.
PA (DOI/) DOBIE K W.
XX
PI Monia BP, Dobie KW;
XX
DR WPI; 2004-340037/31.
XX
PT New compound, having a sequence targeted to a coding region of a nucleic
PT acid encoding human histone deacetylase 2, useful for preparing a
PT composition for treating hyperproliferative disorders, e.g., cancer.
XX
PS Example 15; SEQ ID NO 33; 47bp; English.
XX
CC The invention relates to antisense compounds, compositions and methods
CC for modulating the expression of histone deacetylase 2 (HDAC2). HDAC2 is
CC also known as HDAC-2, hda2, human RPD3 and hRPD3. The composition
CC comprises antisense compounds that can be targeted towards HDAC2. The
CC compound is useful for preparing a composition for treating
CC hyperproliferative disorders, e.g., cancer. It is also useful in
CC antisense gene therapy. The present sequence is an antisense
CC oligonucleotide targeted to human HDAC2 DNA.
XX
SQ Sequence 20 BP; 6 A; 3 C; 4 G; 7 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 12; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 4
ADN49090/c
ID ADN49090 standard; DNA; 20 BP.
XX
AC ADN49090;
XX
DT 15-JUL-2004 (first entry)
XX
DE Human histone deacetylase 2 (HDAC2) DNA target region #14.
XX
KM Histone deacetylase 2; HDAC2; HDAC-2; hda2; RPD3; hRPD3;
KW hyperproliferative disorder; cancer; antisense gene therapy; human; ds;
KW chromosome 6q21.
XX
OS Homo sapiens.
XX
XX
PN US2004077578-A1.
XX
PD 22-APR-2004.
XX
PF 02-SEP-2003; 2003US-00653528.
XX
PR 14-JUN-2002; 2002US-00173192.
XX
PA (MONI/) MONIA B P.
PA (DOI/) DOBIE K W.
XX
PI Monia BP, Dobie KW;
XX
DR WPI; 2004-340037/31.
XX
PT New compound, having a sequence targeted to a coding region of a nucleic
PT acid encoding human histone deacetylase 2, useful for preparing a
PT composition for treating hyperproliferative disorders, e.g., cancer.
XX
PS Example 15; SEQ ID NO 61; 47bp; English.
XX
CC The invention relates to antisense compounds, compositions and methods
CC for modulating the expression of histone deacetylase 2 (HDAC2). HDAC2 is
CC also known as HDAC-2, hda2, human RPD3 and hRPD3. The composition
CC comprises antisense compounds that can be targeted towards HDAC2. The
CC compound is useful for preparing a composition for treating
CC hyperproliferative disorders, e.g., cancer. It is also useful in
CC antisense gene therapy. The present sequence is human HDAC2 DNA target
CC region. Human HDAC2 gene is located at chromosome 6q21.
XX
SQ Sequence 20 BP; 7 A; 4 C; 3 G; 6 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 12; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OY 1 TTATGGAATGATACCGTCAT 20
DB 20 TTATGGAATGATACCGTCAT 1

RESULT 5
ADN27017
ID ADN27017 standard; DNA; 20 BP.
XX
AC ADN27017;
XX
DT 20-MAY-2004 (first entry)
XX
DE Human histone deacetylase 2 DNA antisense oligo, ISIS #157265.
XX
KM Histone deacetylase 2; HDAC2; diagnosis; prevention;
KW hyperproliferative disorder; cancer; apoptosis; metabolic disorder;
KW antisense-therapy; cytostatic; antiinflammatory; human;
KW phosphorothioate backbone; antisense; ss.
XX
OS Homo sapiens.
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C	99	12.2	61.0	51	4
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ALIGNMENTS

RESULT 1
ADJ27016 standard; DNA; 20 BP.

ADJ27016; 20-MAY-2004 (first entry)

Human histone deacetylase 2 DNA antisense oligo, ISIS #157264.

Histone deacetylase 2; HDAC2; diagnosis; prevention; hyperproliferative disorder; cancer; apoptosis; metabolic disorder; antisense-therapy; cytosolic; antineoplastic; human; phosphorothioate backbone; antisense; ss.

Homo sapiens.
Synthetic.

Key
Location/Qualifiers
modified_base 1..20
/tag= b
/mod_base= OTHER
/note= "Phosphorothioate backbone where all cytidines are 5-methyl cytidines"
1..5
/tag= a
/mod_base= OTHER
/note= "2'-methoxyethyl (2'-MOE) nucleotides"
16..20
/tag= c
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US2003236204-A1.
25-DEC-2003.
14-JUN-2002; 2002US-00173192.
14-JUN-2002; 2002US-00173192.
14-JUN-2002; 2002US-00173192.
(ISIS-) ISIS PHARM INC.
Monia BP, Dobie KW;
WPI; 2004-070606/07.

New antisense oligonucleotide compound, useful for diagnosing, preventing and/or treating conditions with aberrant activity of the histone deacetylase 2, such as cancer, inflammation and metabolic disorders.

Example 15; SEQ ID NO 33; 46pp; English.

The present invention relates to antisense compounds, compositions and methods used for modulating histone deacetylase 2 (HDAC2). The methods and compositions of the present invention are useful for the diagnosis, prevention and/or treatment of diseases or conditions associated with aberrant expression or activity of histone deacetylase 2, such as a hyperproliferative disorder (cancer), a condition involving an inflammatory response or an aberrant apoptosis and a metabolic disorder.

CC The invention is also useful in antisense-therapy. The present sequence is human histone deacetylase 2 DNA antisense oligonucleotide used in the exemplification of the invention.

CC Sequence 20 BP; 6 A; 3 C; 4 G; 7 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 12; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTATGATGATACCGTCAT 20
Db 1 TTATGATGATACCGTCAT 20

RESULT 2
ADJ27044/c standard; DNA; 20 BP.

ADJ27044; 20-MAY-2004 (first entry)

Human histone deacetylase 2 target DNA fragment #14.

Histone deacetylase 2; HDAC2; diagnosis; prevention; hyperproliferative disorder; cancer; apoptosis; metabolic disorder; antisense-therapy; cytosolic; antineoplastic; human; ds.

Homo sapiens.
US2003236204-A1.
25-DEC-2003.
14-JUN-2002; 2002US-00173192.
14-JUN-2002; 2002US-00173192.
(ISIS-) ISIS PHARM INC.
Monia BP, Dobie KW;
WPI; 2004-070606/07.

New antisense oligonucleotide compound, useful for diagnosing, preventing and/or treating conditions with aberrant activity of the histone deacetylase 2, such as cancer, inflammation and metabolic disorders.

Example 15; SEQ ID NO 61; 46pp; English.

The present invention relates to antisense compounds, compositions and methods used for modulating histone deacetylase 2 (HDAC2). The methods and compositions of the present invention are useful for the diagnosis, prevention and/or treatment of diseases or conditions associated with aberrant expression or activity of histone deacetylase 2, such as a hyperproliferative disorder (cancer), a condition involving an inflammatory response or an aberrant apoptosis and a metabolic disorder. The invention is also useful in antisense-therapy. The present sequence is human histone deacetylase 2 target DNA fragment used in the exemplification of the invention.

Sequence 20 BP; 7 A; 4 C; 3 G; 6 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 12; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTATGATGATACCGTCAT 20
Db 20 TTATGATGATACCGTCAT 1

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 1, 2006, 22:25:00 ; Search time 336.667 Seconds
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Scoring table: IDENTITY NUC
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Minimum DB seq length: 0
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Listing first 100 summaries

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14: geneseqn2005s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	20	100.0	20	12	ADJ27044 Human his
3	20	100.0	20	12	ADN49062 Human HDA
4	20	100.0	20	12	ADN49090 Human his
5	19	95.0	20	12	ADJ27017 Human his
6	19	95.0	20	12	ADN49063 Human HDA
7	16.8	84.0	60	14	ABE27395 P. radiat
8	15.2	76.0	20	13	ADR55403 Human HDA
9	14.2	71.0	22	2	AAT86745 PCR prime
10	14.2	71.0	22	2	AAT86857 Raspberry
11	14.2	71.0	26	4	AAC87300 Yersinia
12	13.8	69.0	20	10	ABE92294 Human oli
13	13.8	69.0	20	11	ABD28524 R1463-de
14	13.8	69.0	30	13	ADR99683 Chlamydia
15	13.8	69.0	54	6	AAD39714 Synthetic
16	13.8	69.0	80	6	AAD39720 Synthetic
17	13.8	69.0	80	12	ADM79905 DNA ligan
18	13.6	68.0	47	3	AAZ67315 Human map
19	13.6	68.0	50	6	ABZ03677 Human leu

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29	13.2	66.0	50	6	ABZ03124	Abz03124 Human leu
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47	12.6	63.0	31	3	AAZ73252	Aaz73252 Consensus
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52	12.6	63.0	43	12	ADP96898	Adp96898 C. albica
53	12.6	63.0	47	3	AAZ69660	Aaz69660 Human map
54	12.6	63.0	60	14	ADZ60454	Adz60454 Rat 60052
55	12.6	63.0	60	14	AEA07604	Aea07604 DNA micro
56	12.6	63.0	65	6	ABZ29171	Abz29171 Candida g
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58	12.6	63.0	65	12	ADP97738	Adp97738 C. albica
59	12.6	63.0	71	2	AAZ058575	Aaz058575 Listeria
60	12.6	63.0	71	2	AAQ48011	Aaq48011 Listeria
61	12.6	63.0	71	14	AEA29666	Aea29666 p2JM103-B
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TITLE Biallelic markers for use in constructing a high density
disequilibrium map of the human genome
JOURNAL Patent: US 6537751-A 1307 25-MAR-2003;
Genet S.A.;;

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ORIGIN

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Best Local Similarity 78.9%; Pred. No. 3.4e+05;
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| | | | | | | | | | | | | | | | | | | | | |
Db 1 TCTGTATGATACGTTTCAT 19

Search completed: March 1, 2006, 22:55:13
Job time : 594.333 secs

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VERSION	AR361595.1	GI:33769464					
KEYWORDS							
SOURCE	Unknown.						
ORGANISM	Unclassified.						
REFERENCE	1 (bases 1 to 31)						
AUTHORS	Barok,A., Mueh,T. and Rueckel,M.						
TITLE	Continuous fermentation system						
JOURNAL	Patent: US 6599735-A 28 29-JUL-2003;						
	Roche Vitamins Inc.; Parsippany, NJ;						
	EPX;						
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29	TTCTGGAATGATCAAGTTA	11					
RESULT 23							
LOCUS	AR361596			31 bp	DNA	linear	PAT 17-AUG-2003
DEFINITION	Sequence 29 from patent US 6599735.						
ACCESSION	AR361596						
VERSION	AR361596.1	GI:33769465					
KEYWORDS							
SOURCE	Unknown.						
ORGANISM	Unclassified.						
REFERENCE	1 (bases 1 to 31)						
AUTHORS	Bartok,A., Mueh,T. and Rueckel,M.						
TITLE	Continuous fermentation system						
JOURNAL	Patent: US 6599735-A 29 29-JUL-2003;						
	Roche Vitamins Inc.; Parsippany, NJ;						
	EPX;						
FEATURES	Location/Qualifiers						
source	1..31						
	/organism="unknown"						
	/mol_type="genomic DNA"						
ORIGIN							
Query Match	63.0%;	Score 12.6;	DB 6;				
Best Local Similarity	78.9%;	Pred. No. 3.7e+05;					
Matches	15;	Conservative 0;	Mismatches 4;				
1	TTATGAAATGATACCGTCA	19					
3	TTCTGGAATGATCAAGTTA	21					
RESULT 24							
LOCUS	AR494427			31 bp	DNA	linear	PAT 15-MAY-2004
DEFINITION	Sequence 52 from patent US 6720174.						
ACCESSION	AR494427						
VERSION	AR494427.1	GI:47268592					
KEYWORDS							
SOURCE	Unknown.						
ORGANISM	Unclassified.						

REFERENCE	Unclassified.
AUTHORS	1 (bases 1 to 31)
TITLE	Lehmann,M.
JOURNAL	Phytases Patent: US 6720174-A 52 13-APR-2004; Novozymes A/S and Roche Vitamins Inc.; Bagsvaerd; DKX;
FEATURES	Location/Qualifiers 1..31
SOURCE	/organism="unknown" /mol_type="genomic DNA"
ORIGIN	
Query Match	63.0%; Score 12.6; DB 6; Length 31;
Best Local Similarity	78.9%; Pred. No. 3.7e+05;
Matches	15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
OY	1 TTATGAATGATACCGTCA 19
Db	29 TTCTGAATGATCACGTTA 11
RESULT 25	
LOCUS	AX137177/c 31 bp DNA linear PAT 30-MAY-2001
DEFINITION	Sequence 28 from Patent EPI092764.
ACCESSION	AX137177
VERSION	AX137177.1 GI:14273503
KEYWORDS	.
SOURCE	synthetic construct
ORGANISM	synthetic construct
REFERENCE	other sequences; artificial sequences.
AUTHORS	1
TITLE	Bartok,A., Mueh,T. and Rueckel,M.
JOURNAL	Continuous fermentation process Patent: EP 1092764-A 28 18-APR-2001; F. HOFFMANN-LA ROCHE AG (CH) Location/Qualifiers 1..31
FEATURES	/organism="synthetic construct" /mol_type="unassigned DNA" /db_xref="taxon:32630" /note="Primer"
SOURCE	
ORIGIN	
Query Match	63.0%; Score 12.6; DB 6; Length 31;
Best Local Similarity	78.9%; Pred. No. 3.7e+05;
Matches	15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
OY	1 TTATGAATGATACCGTCA 19
Db	29 TTCTGAATGATCACGTTA 11
RESULT 26	
LOCUS	AX137178 31 bp DNA linear PAT 30-MAY-2001
DEFINITION	Sequence 29 from Patent EPI092764.
ACCESSION	AX137178
VERSION	AX137178.1 GI:14273504
KEYWORDS	.
SOURCE	synthetic construct
ORGANISM	synthetic construct
REFERENCE	other sequences; artificial sequences.
AUTHORS	1
TITLE	Bartok,A., Mueh,T. and Rueckel,M.
JOURNAL	Continuous fermentation process Patent: EP 1092764-A 29 18-APR-2001; F. HOFFMANN-LA ROCHE AG (CH) Location/Qualifiers 1..31
FEATURES	/organism="synthetic construct" /mol_type="unassigned DNA"
SOURCE	

Db 24 TTATGATGATGATA 12

RESULT 18
AX181005/c
LOCUS AX181005 25 bp DNA linear PAT 06-AUG-2001
DEFINITION Sequence 56 from Patent WO0145493.
ACCESSION AX181005
VERSION AX181005.1 GI:15132788
KEYWORDS
SOURCE
ORGANISM
synthetic construct
other sequences; artificial sequences.

REFERENCE
AUTHORS
TITLE
JOURNAL
Plants: WO 0145493-A 56 28-JUN-2001;
Patent: BASF Plant Science GmbH (DE)
Location/Qualifiers
1..25
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Primer"

ORIGIN
Query Match 64.0%; Score 12.8; DB 6; Length 25;
Best Local Similarity 87.5%; Pred. No. 3e+05; 2; Indels 0; Gaps 0;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 ATGAGATGATACCGTC 18
|||||
19 ATGGGTGATACCGTC 4

Db 19 ATGGGTGATACCGTC 4

RESULT 19
I32151
LOCUS I32151 60 bp DNA linear PAT 06-FEB-1997
DEFINITION Sequence 5 from patent US 5585256.
ACCESSION I32151
VERSION I32151.1 GI:1822942
KEYWORDS
SOURCE
ORGANISM
Unknown.
Unclassified.

REFERENCE
AUTHORS
TITLE
JOURNAL
Patent: US 5585256-A 5 17-DEC-1996;
Location/Qualifiers
1..60
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 64.0%; Score 12.8; DB 6; Length 60;
Best Local Similarity 87.5%; Pred. No. 2.6e+05; 2; Indels 0; Gaps 0;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 TGAATGATACCGTCA 19
|||||
21 TGAATGCCACCGTCA 36

Db 21 TGAATGCCACCGTCA 36

RESULT 20
CS075741
LOCUS CS075741 21 bp RNA linear PAT 06-MAY-2005
DEFINITION Sequence 158 from Patent WO2005036176.
ACCESSION CS075741

VERSION CS075741.1 GI:63092478
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.

REFERENCE
AUTHORS
TITLE
JOURNAL
Cell surface molecules as markers and therapeutic agents against
kidney cancers
Patent: WO 2005036176-A 158 21-APR-2005;
Myeth (US)
Location/Qualifiers
1..21
/organism="Homo sapiens"
/mol_type="unassigned RNA"
/db_xref="taxon:9606"

ORIGIN
Query Match 63.0%; Score 12.6; DB 6; Length 21;
Best Local Similarity 78.9%; Pred. No. 3.3e+05; 4; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 TTATGATGATACCGTCA 19
|||||
1 TTACGGAATGTGCTTCA 19

Db 1 TTACGGAATGTGCTTCA 19

RESULT 21
BD243302/c
LOCUS BD243302 31 bp DNA linear PAT 17-JUL-2003
DEFINITION Improved phytases.
ACCESSION BD243302
VERSION BD243302.1 GI:33053072
KEYWORDS
SOURCE
ORGANISM
synthetic construct
other sequences; artificial sequences.

REFERENCE
AUTHORS
TITLE
JOURNAL
Patent: JP 2002534976-A 22 22-OCT-2002;
NOVOZYMES AS
OS Artificial Sequence
PN JP 2002534976-A/22
PD 22-OCT-2002
PR 21-JAN-2000 JP 2000594911
PT 22-JAN-1999 DK PA 199900092.21-SEP-1999 DK PA 199901340 PI
MARTIN LEMANN, SOANE FLEHNSTED LASSSEN
PC C12N15/09, A23K1/165, A23L1/30, A61K38/46, A61P43/00, C12N1/15, PC
C12N1/19,
PC C12N1/21, C12N5/10, C12N9/16, C12N9/16, C12R1.865, C12N9/16, PC
C12R1.685)
PC C12N15/00, C12N5/00, A61K37/54
CC Description of Artificial Sequence: primer
FH Key Location/Qualifiers
FT source 1..31
FT
Location/Qualifiers
1..31
/organism="Artificial Sequence".
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

ORIGIN
Query Match 63.0%; Score 12.6; DB 6; Length 31;
Best Local Similarity 78.9%; Pred. No. 3.7e+05; 4; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 TTATGATGATACCGTCA 19
|||||
29 TTCTGATGATGATGCTTCA 11

Db 29 TTCTGATGATGATGCTTCA 11

FEATURES
source
Location/Qualifiers
1..41
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match 66.0%; Score 13.2; DB 6; Length 41;
Best Local Similarity 75.0%; Pred. No. 1.7e+05;
Matches 15; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 TTATGAATGATACCGTCAT 20
Db 31 TTATGTAACRCACTGCTT 12

RESULT 14
LOCUS CQ538756 60 bp DNA linear PAT 30-JAN-2004
DEFINITION Sequence 8391 from Patent WO0210449.
ACCESSION CQ538756
VERSION CQ538756.1 GI:41505020
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.

REFERENCE
AUTHORS Shoshan,A., Maeserman,A., Mintz,E., Mintz,L. and Faigler,S.
TITLE Oligonucleotide library for detecting rna transcripts and splice
JOURNAL variants that populate a transcriptome
Patent: WO 0210449-A 8391 07-FEB-2002;
Compugen Inc. (US)

FEATURES
source
Location/Qualifiers
1..60
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match 66.0%; Score 13.2; DB 6; Length 60;
Best Local Similarity 83.3%; Pred. No. 1.6e+05;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 ATGAATGATACCGTCAT 20
Db 5 ATGAATGATGACTTCAT 22

RESULT 15
LOCUS CQ547491 60 bp DNA linear PAT 30-JAN-2004
DEFINITION Sequence 17126 from Patent WO0210449.
ACCESSION CQ547491
VERSION CQ547491.1 GI:41513755
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.

REFERENCE
AUTHORS Shoshan,A., Maeserman,A., Mintz,E., Mintz,L. and Faigler,S.
TITLE Oligonucleotide library for detecting rna transcripts and splice
JOURNAL variants that populate a transcriptome
Patent: WO 0210449-A 17126 07-FEB-2002;
Compugen Inc. (US)

FEATURES
source
Location/Qualifiers
1..60
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match 66.0%; Score 13.2; DB 6; Length 60;
Best Local Similarity 83.3%; Pred. No. 1.6e+05;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 TTATGAATGATACCGTCA 19
Db 4 TTGGATGATACCCACA 21

RESULT 16
LOCUS CQ51589/c 60 bp DNA linear PAT 30-JAN-2004
DEFINITION Sequence 21224 from Patent WO0210449.
ACCESSION CQ51589
VERSION CQ51589.1 GI:41518016
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.

REFERENCE
AUTHORS Shoshan,A., Maeserman,A., Mintz,E., Mintz,L. and Faigler,S.
TITLE Oligonucleotide library for detecting rna transcripts and splice
JOURNAL variants that populate a transcriptome
Patent: WO 0210449-A 21224 07-FEB-2002;
Compugen Inc. (US)

FEATURES
source
Location/Qualifiers
1..60
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match 66.0%; Score 13.2; DB 6; Length 60;
Best Local Similarity 83.3%; Pred. No. 1.6e+05;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 TATGAATGATACCGTCA 19
Db 39 TATGGCATGATACAGCA 22

RESULT 17
LOCUS AX054735/c 28 bp DNA linear PAT 13-JAN-2001
DEFINITION Sequence 39 from Patent WO073438.
ACCESSION AX054735
VERSION AX054735.1 GI:12228255
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.

REFERENCE
1 Adolf,G., Heider,K.H., Koenig,U. and Sommergruber,W.
Tumor-associated antigen (c42)
Patent: WO 0073438-A 39 07-DEC-2000;
BOEHRINGER INGELHEIM VETMEDICA GMBH (DE)

FEATURES
source
Location/Qualifiers
1..28
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Primer"

ORIGIN
Query Match 65.0%; Score 13; DB 6; Length 28;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTATGAATGATA 13

TITLE Human gene RecQ4 encoding helicase
JOURNAL Patent: US 6472513-A 25 29-OCT-2002;
Agene Research Institute Co., Ltd.; Kanagawa;
JPX;
FEATURES
source Location/Qualifiers
1..24
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN
Query Match 66.0%; Score 13.2; DB 6; Length 24;
Best Local Similarity 83.3%; Pred. No. 1.9e+05;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1 TTATGGAATGATACCGTC 18
| | | | | | | | | | | | | | | | | | | | | |
5 TCATGGAATGATCCTGTC 22
Db
RESULT 10
BD012839 24 bp DNA linear PAT 02-AUG-2002
LOCUS Nucleus localizing RecQ5-type DNA helicase.
DEFINITION BD012839
ACCESSION BD012839
VERSION BD012839.1 GI:22093028
KEYWORDS WO 0125425-A/12.
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE
1 (bases 1 to 24)
Furuchi, Y., Shimamoto, A., Kitao, S. and Nishikawa, K.
Nucleus localizing RecQ5-type DNA helicase
Patent: WO 0125425-A 12 12-APR-2001;
AGENE RESEARCH INSTITUTE CO LTD, YASUHIRO FURUCHI, AKIRA SHIMAMOTO,
SAORI KITAO, KAORI NISHIKAWA
COMMENT OS Artificial Sequence
PN WO 0125425-A/12
PD 12-APR-2001
PF 25-AUG-2000 WO 2000JP005757
PR 05-OCT-1999 JP 99P 284001
PI YASUHIRO FURUCHI, AKIRA SHIMAMOTO, SAORI KITAO, KAORI NISHIKAWA
PC C12N15/12, C12N9/14, C12Q1/68, C07K16/18, G01N33/53, A01K67/00 CC
Description of Artificially Synthesized CC
Primer Sequence
FH Key Location/Qualifiers.
FEATURES
source 1..24
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
ORIGIN
Query Match 66.0%; Score 13.2; DB 6; Length 24;
Best Local Similarity 83.3%; Pred. No. 1.9e+05;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1 TTATGGAATGATACCGTC 18
| | | | | | | | | | | | | | | | | | | | | |
5 TCATGGAATGATCCTGTC 22
Db
RESULT 11
AX598464 26 bp DNA linear PAT 14-FEB-2003
LOCUS Sequence 738 from Patent WO0244994.
DEFINITION AX598464
ACCESSION AX598464
VERSION AX598464.1 GI:28398640
KEYWORDS
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE
1 Brower, A., Brow, M.A., Cracauer, R.F., Fors, L., Granske, R., de arruda

Indig, M., Kurensky, D., Luedtke, C., Lukowiak, A.A., Lyamichev, V.,
Meri, B.P., Reimer, N.D., Roeven, R.T., Skrzypczynski, Z., Ziarno, W.A.,
Cometford, J., Stump, S. and Viegut, D.D.
Systems and method for detection assay production and sale
Patent: WO 0244994-A 738 06-JUN-2002;
THIRD WAVE TECHNOLOGIES, INC. (US)
FEATURES
source Location/Qualifiers
1..26
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
ORIGIN
Query Match 66.0%; Score 13.2; DB 6; Length 26;
Best Local Similarity 83.3%; Pred. No. 1.9e+05;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1 TTATGGAATGATACCGTC 18
| | | | | | | | | | | | | | | | | | | | | |
4 TTTTGAATGATGACCGTC 21
Db
RESULT 12
AX598492 26 bp DNA linear PAT 14-FEB-2003
LOCUS Sequence 766 from Patent WO0244994.
DEFINITION AX598492
ACCESSION AX598492
VERSION AX598492.1 GI:28398670
KEYWORDS
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE
1
Brower, A., Brow, M.A., Cracauer, R.F., Fors, L., Granske, R., de arruda
Indig, M., Kurensky, D., Luedtke, C., Lukowiak, A.A., Lyamichev, V.,
Meri, B.P., Reimer, N.D., Roeven, R.T., Skrzypczynski, Z., Ziarno, W.A.,
Cometford, J., Stump, S. and Viegut, D.D.
Systems and method for detection assay production and sale
Patent: WO 0244994-A 766 06-JUN-2002;
THIRD WAVE TECHNOLOGIES, INC. (US)
FEATURES
source 1..26
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
ORIGIN
Query Match 66.0%; Score 13.2; DB 6; Length 26;
Best Local Similarity 83.3%; Pred. No. 1.9e+05;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1 TTATGGAATGATACCGTC 18
| | | | | | | | | | | | | | | | | | | | | |
4 TTTTGAATGATGACCGTC 21
Db
RESULT 13
AX518177 41 bp DNA linear PAT 05-OCT-2002
LOCUS Sequence 4375 from Patent WO0205044.
DEFINITION AX518177
ACCESSION AX518177
VERSION AX518177.1 GI:23567516
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
REFERENCE
1 Nakamura, Y., Sekine, A., Iida, A. and Saito, S.
Detection of genetic polymorphisms
Patent: WO 02052044-A 4375 04-JUL-2002;
Riken (JP)

SOURCE Candida albicans
ORGANISM Candida albicans
REFERENCE Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; mitosporic Saccharomycetales; Candida.
1
AUTHORS Roemer, T., Jiang, B., Boone, C., Bussey, H. and Ohlsen, K.L.
TITLE Gene disruption methodologies for drug target discovery
JOURNAL Patent: WO 02053728-A 3166 11-JUL-2002;
Elitra Pharmaceuticals, Inc. (US)
FEATURES Location/Qualifiers
source 1..65
/organism="Candida albicans"
/mol_type="unassigned DNA"
/db_xref="taxon:5476"
ORIGIN
Query Match 68.0%; Score 13.6; DB 6; Length 65;
Best Local Similarity 80.0%; Pred. No. 1e+05;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 TTATGAAATGATACCGTCAT 20
19 TTACTGAAGATACCGTCTT 38
Db
RESULT 6 CS064922 21 bp DNA linear PAT 20-APR-2005
LOCUS Sequence 270 from Patent WO2005031004.
DEFINITION CS064922
ACCESSION CS064922.1 GI:62817779
VERSION
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE other sequences; artificial sequences.
1
AUTHORS Snaidr, J., Beinhof, C., Theisen, K. and Lehner, A.
TITLE Method for the specific rapid detection of beverage-spoiling
JOURNAL micro-organisms
Patent: WO 2005031004-A 270 07-APR-2005;
Vermicon AG (DE)
FEATURES Location/Qualifiers
source 1..21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="oligonucleotide"
ORIGIN
Query Match 66.0%; Score 13.2; DB 6; Length 21;
Best Local Similarity 83.3%; Pred. No. 1.9e+05;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 TTATGAAATGATACCGTC 18
4 TTCTGGATGTATCCGTC 21
Db
RESULT 7 E30500 24 bp DNA linear PAT 18-JUN-2001
E30500
LOCUS Gene RecQ5 encoding helicase.
DEFINITION E30500
ACCESSION E30500.1 GI:13021449
VERSION JP 1999276173-A/22.
KEYWORDS unidentifed
SOURCE unidentifed
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 24)
AUTHORS Saori, K., Akira, S. and Yasuniro, F.
TITLE Gene RecQ5 encoding helicase
JOURNAL Patent: JP 1999276173-A 22 12-OCT-1999;
AGENE RES INSTI CO LTD

COMMENT OS Unidentified
PN JP 1999276173-A/22
PD 12-OCT-1999
PF 27-MAR-1998 JP 1998081492
PR
PI SAORI KITAO, AKIRA SHIMAMOTO, YASUHIRO FURUTCHI PC
C12N15/09, A01K67/027, C07K16/40, C12N5/10, C12N9/00, C12P21/02, PC
C12P21/08,
PC C1201/68, G01N33/50, G01N33/53, G01N33/577// (C12N15/09, C12R1:91),
PC (C12N5/10, C12R1:91) (C12P21/08, C12R1:91), C12N15/00, C12N5/00,
PC (C12N15/00, C12R1:91), (C12N5/00, C12R1:91)
CC Strandedness: Single;
CC Topology: Linear;
FH Key
FH source 1..24
FT Location/Qualifiers
FEATURES
source 1..24
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
ORIGIN
Query Match 66.0%; Score 13.2; DB 6; Length 24;
Best Local Similarity 83.3%; Pred. No. 1.9e+05;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 TTATGAAATGATACCGTC 18
5 TCATGGAATGATCTGTC 22
Db
RESULT 8 AR181902 24 bp DNA linear PAT 20-APR-2002
AR181902
LOCUS Sequence 25 from patent US 6335435.
DEFINITION AR181902
ACCESSION AR181902
VERSION AR181902.1 GI:20224116
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
1 (bases 1 to 24)
AUTHORS Shimamoto, A., Kitao, S. and Furuchi, Y.
TITLE Human gene RecQ4 encoding helicase
JOURNAL Patent: US 6335435-A 25 01-JAN-2002;
FEATURES Location/Qualifiers
source 1..24
/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN
Query Match 66.0%; Score 13.2; DB 6; Length 24;
Best Local Similarity 83.3%; Pred. No. 1.9e+05;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 TTATGAAATGATACCGTC 18
5 TCATGGAATGATCTGTC 22
Db
RESULT 9 AR242516 24 bp DNA linear PAT 20-DEC-2002
AR242516
LOCUS Sequence 25 from patent US 6472513.
DEFINITION AR242516
ACCESSION AR242516
VERSION AR242516.1 GI:27288961
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
1 (bases 1 to 24)
AUTHORS Shimamoto, A., Kitao, S. and Furuchi, Y.

C 92 12 60.0 42 6 128221 128221 Sequence 2
C 93 12 60.0 42 6 128223 128223 Sequence 2
C 94 12 60.0 42 6 128843 128843 Sequence 2
C 95 12 60.0 42 6 130487 130487 Sequence 2
C 96 12 60.0 42 6 133928 133928 Sequence 4
C 97 12 60.0 42 6 133954 133954 Sequence 2
C 98 12 60.0 42 6 136323 136323 Sequence 2
C 99 12 60.0 42 6 138381 138381 Sequence 2
C 100 12 60.0 42 6 176418 176418 Sequence 2

ALIGNMENTS

RESULT 1
AR019213/c AR019213 22 bp DNA linear PAT 05-DEC-1998

LOCUS AR019213
DEFINITION Sequence 7 from patent US 5783393.
ACCESSION AR019213
VERSION AR019213.1 GI:3974327
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE
AUTHORS 1 (bases 1 to 22)
TITLE Kelllogg, J. Anne, and Bestwick, R. Keith.
JOURNAL Plant tissue/stage specific promoters for regulated expression of
FEATURES transgenes in plants
source Location/Qualifiers
1..22
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

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Best Local Similarity 84.2%; Pred. No. 5.9e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 TTATGATGATACCGTCA 19
Db 20 TTATGACTAATACCGTCA 2

RESULT 2

AR019246/c AR019246 22 bp DNA linear PAT 05-DEC-1998
LOCUS AR019246
DEFINITION Sequence 18 from patent US 5783394.
ACCESSION AR019246
VERSION AR019246.1 GI:3974360
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE
AUTHORS 1 (bases 1 to 22)
TITLE Bestwick, R.K. and Kelllogg, J. Anne.
JOURNAL Rasperberry promoters for expression of transgenes in plants
FEATURES Patent: US 5783394-A 18 21-JUL-1998;
source Location/Qualifiers
1..22
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 71.0%; Score 14.2; DB 6; Length 22;
Best Local Similarity 84.2%; Pred. No. 5.9e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 TTATGATGATACCGTCA 19
Db 20 TTATGACTAATACCGTCA 2

RESULT 3
CQ868111 CQ868111 30 bp DNA linear PAT 13-SEP-2004
LOCUS CQ868111
DEFINITION Sequence 328 from Patent WO2004074318.
ACCESSION CQ868111
VERSION CQ868111.1 GI:51998163
KEYWORDS
SOURCE Synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.

REFERENCE
AUTHORS 1
TITLE Dautry-Varsat, A. and Subtil-Sands, A.
JOURNAL Secreted chlamydia polypeptides, polynucleotides coding
therefor, therapeutic and diagnostic uses thereof
Patent: WO 2004074318-A 328 02-SEP-2004;
INSTITUT PASTEUR (FR); CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE
(CNRS) (FR)

FEATURES
source Location/Qualifiers
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic DNA"

ORIGIN

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Best Local Similarity 88.2%; Pred. No. 9e+04;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 3 ATGCAATGATATTCGTCA 19
Db 10 ATGCAATGATATTCGTCA 26

RESULT 4

AR289927 AR289927 47 bp DNA linear PAT 12-JUN-2003
LOCUS AR289927
DEFINITION Sequence 1662 from patent US 6537751.
ACCESSION AR289927
VERSION AR289927.1 GI:31677211
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE
AUTHORS 1 (bases 1 to 47)
TITLE Cohen, D., Chumakov, I. and Blumenfeld, M.
JOURNAL Biallelic markers for use in constructing a high density
Patent: US 6537751-A 1662 25-MAR-2003;
Genet. S.A.;;
FRX;

FEATURES
source Location/Qualifiers
1..47
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

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Best Local Similarity 80.0%; Pred. No. 1.1e+05;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 TTATGATGATACCGTCAT 20
Db 27 TTATATAAAGATTCGTCAT 46

RESULT 5

AX485866 AX485866 65 bp DNA linear PAT 16-AUG-2002
LOCUS AX485866
DEFINITION Sequence 3166 from Patent WO02053728.
ACCESSION AX485866
VERSION AX485866.1 GI:22320082
KEYWORDS

KEYWORDS

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 1, 2006, 22:25:24 ; Search time 589.333 Seconds
(without alignments)
1929.076 Million cell updates/sec

Title: US-10-653-528-33
Perfect score: 20
Sequence: 1 ttatcggaatgatacgcgtcat 20

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 5883141 segs, 28421725653 residues
Total number of hits satisfying chosen parameters: 2389942

Minimum DB seq length: 0
Maximum DB seq length: 80

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database :

GenBml: *
1: gb_ha: *
2: gb_in: *
3: gb_env: *
4: gb_om: *
5: gb_ov: *
6: gb_pat: *
7: gb_ph: *
8: gb_pr: *
9: gb_ro: *
10: gb_sts: *
11: gb_sy: *
12: gb_un: *
13: gb_vl: *
14: gb_htg: *
15: gb_pl: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	14.2	71.0	22	6	AR019213 Sequence
C 2	14.2	71.0	22	6	AR019246 Sequence
C 3	13.8	69.0	30	6	CO868111 Sequence
C 4	13.6	68.0	47	6	AR289927 Sequence
C 5	13.6	68.0	65	6	AX485866 Sequence
C 6	13.2	66.0	21	6	CS064922 Sequence
C 7	13.2	66.0	24	6	E30500 Sequence
C 8	13.2	66.0	24	6	AR181902 Sequence
C 9	13.2	66.0	24	6	AR242516 Sequence
C 10	13.2	66.0	24	6	BD012839 Sequence
C 11	13.2	66.0	26	6	AX588464 Sequence
C 12	13.2	66.0	26	6	AX598492 Sequence
C 13	13.2	66.0	41	6	AX518177 Sequence
C 14	13.2	66.0	60	6	CO538756 Sequence
C 15	13.2	66.0	60	6	CO547491 Sequence
C 16	13.2	66.0	60	6	CO551589 Sequence
C 17	13.2	65.0	28	6	AX054735 Sequence
C 18	12.8	64.0	25	6	AX181005 Sequence

19	12.8	64.0	60	6	I32151	I32151 Sequence 5
20	12.6	63.0	21	6	CS075741	CS075741 Sequence
C 21	12.6	63.0	31	6	BD243302	BD243302 Improved
C 22	12.6	63.0	31	6	AR361595	AR361595 Sequence
C 23	12.6	63.0	31	6	AR361596	AR361596 Sequence
C 24	12.6	63.0	31	6	AR494427	AR494427 Sequence
C 25	12.6	63.0	31	6	AX137177	AX137177 Sequence
C 26	12.6	63.0	31	6	AX137178	AX137178 Sequence
C 27	12.6	63.0	31	6	BD015101	BD015101 Continou
C 28	12.6	63.0	31	6	BD015102	BD015102 Continou
C 29	12.6	63.0	33	6	CO816210	CO816210 Sequence
C 30	12.6	63.0	47	6	AR289572	AR289572 Sequence
C 31	12.6	63.0	56	4	BTRBP6	V00130 Bovine sal
C 32	12.6	63.0	60	6	CS102525	CS102525 Sequence
C 33	12.6	63.0	65	6	AX485954	AX485954 Sequence
C 34	12.6	63.0	71	6	CS103417	CS103417 Sequence
C 35	12.6	63.0	71	6	B05341	E05341 Libertia mo
C 36	12.6	63.0	79	6	CS103416	CS103416 Sequence
C 37	12.6	63.0	80	8	S49226	S49226 {DX525 10c
C 38	12.4	62.0	37	6	AR224493	E10314 PCR primer
C 39	12.2	61.0	19	6	AR574586	AR574586 Sequence
C 40	12.2	61.0	19	6	AX132696	AX132696 Sequence
C 41	12.2	61.0	20	6	CQ790243	CQ790243 Sequence
C 42	12.2	61.0	20	6	AX716866	AX716866 Sequence
C 43	12.2	61.0	21	6	AR393560	AR393560 Sequence
C 44	12.2	61.0	21	6	BD262063	BD262063 Antineopl
C 45	12.2	61.0	22	6	AR303037	AR303037 Sequence
C 46	12.2	61.0	22	6	AX036797	AX036797 Sequence
C 47	12.2	61.0	24	6	AR053869	AR053869 Sequence
C 48	12.2	61.0	24	6	E25304	E25304 Novel aspar
C 49	12.2	61.0	24	6	AX288973	AX288973 Sequence
C 50	12.2	61.0	24	6	BD017598	BD017598 Novel asp
C 51	12.2	61.0	25	6	AR090645	AR090645 Sequence
C 52	12.2	61.0	25	6	AR197680	AR197680 Sequence
C 53	12.2	61.0	25	6	AR259834	AR259834 Sequence
C 54	12.2	61.0	29	6	A56672	A56672 Sequence 6
C 55	12.2	61.0	29	6	AR051606	AR051606 Sequence
C 56	12.2	61.0	31	6	AX577727	AX577727 Sequence
C 57	12.2	61.0	32	6	CS062999	CS062999 Sequence
C 58	12.2	61.0	32	6	AX665973	AX665973 Sequence
C 59	12.2	61.0	34	6	AX742062	AX742062 Sequence
C 60	12.2	61.0	36	6	A56681	A56681 Sequence 15
C 61	12.2	61.0	36	6	AR051615	AR051615 Sequence
C 62	12.2	61.0	38	6	AX742063	AX742063 Sequence
C 63	12.2	61.0	51	6	CQ001957	CQ001957 Sequence
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C 65	12.2	61.0	51	6	AX158357	AX158357 Sequence
C 66	12.2	61.0	51	6	AX158358	AX158358 Sequence
C 67	12.2	61.0	59	6	AX523091	AX523091 Sequence
C 68	12.2	61.0	60	6	BD180865	BD180865 Array of
C 69	12.2	61.0	70	6	AR403960	AR403960 Sequence
C 70	12.2	61.0	21	6	CS011428	CS011428 Sequence
C 71	12.2	60.0	28	10	CR378952	CR378952 Arabidops
C 72	12.2	60.0	30	6	AX791874	AX791874 Sequence
C 73	12.2	60.0	32	6	AR098076	AR098076 Sequence
C 74	12.2	60.0	39	6	AR009789	AR009789 Sequence
C 75	12.2	60.0	40	6	E50142	E50142 Porous holl
C 76	12.2	60.0	42	6	AR009788	AR009788 Sequence
C 77	12.2	60.0	42	6	AR068045	AR068045 Sequence
C 78	12.2	60.0	42	6	I21413	I21413 Sequence 2
C 79	12.2	60.0	42	6	I22037	I22037 Sequence 2
C 80	12.2	60.0	42	6	I23412	I23412 Sequence 2
C 81	12.2	60.0	42	6	I25839	I25839 Sequence 2
C 82	12.2	60.0	42	6	I25841	I25841 Sequence 3
C 83	12.2	60.0	42	6	I25843	I25843 Sequence 3
C 84	12.2	60.0	42	6	I25882	I25882 Sequence 3
C 85	12.2	60.0	42	6	I26710	I26710 Sequence 3
C 86	12.2	60.0	42	6	I27183	I27183 Sequence 2
C 87	12.2	60.0	42	6	I27185	I27185 Sequence 2
C 88	12.2	60.0	42	6	I27187	I27187 Sequence 2
C 89	12.2	60.0	42	6	I27816	I27816 Sequence 2
C 90	12.2	60.0	42	6	I27826	I27826 Sequence 2
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; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 164831
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-164831

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Query Match          71.0%; Score 14.2; DB 11; Length 19;
Best Local Similarity 63.2%; Pred. No. 7.2e+02;
Matches 12; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

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; Sequence 164932, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dnarmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 164932
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-164932

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Query Match          71.0%; Score 14.2; DB 11; Length 19;
Best Local Similarity 63.2%; Pred. No. 7.2e+02;
Matches 12; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

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QY      1 ATAAAGCTTCTTCAACA 19
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US-11-101-244-453541
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Best Local Similarity 63.2%; Pred. No. 7.2e+02;
Matches 12; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
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RESULT 26

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US-11-101-244-572442/C
; Sequence 572442, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 572442
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-572442
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Query Match          71.0%; Score 14.2; DB 10; Length 19;
Best Local Similarity 84.2%; Pred. No. 7.2e+02;
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RESULT 27

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US-11-083-784-164632
; Sequence 164632, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
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; NUMBER OF SEQ ID NOS: 1591911
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; SEQ ID NO 164632
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-164632
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Best Local Similarity 63.2%; Pred. No. 7.2e+02;
Matches 12; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
```

```
Qy      1 ATAAAGCTCTTCAACA 19
        |||||:::|::|
Db      1 AUAAGAGCUCUCCAAUA 19
```

RESULT 28

```
US-11-083-784-164732
; Sequence 164732, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
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; SEQ ID NO 164732
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-164732
```

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Query Match          71.0%; Score 14.2; DB 11; Length 19;
Best Local Similarity 63.2%; Pred. No. 7.2e+02;
Matches 12; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
```

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Qy      1 ATAAAGCTCTTCAACA 19
        |||||:::|::|
Db      1 AUAAGAGCUCUCCAAUA 19
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RESULT 29

```
US-11-083-784-164831
; Sequence 164831, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
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; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
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; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-164831
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```
Query Match          71.0%; Score 14.2; DB 10; Length 19;
Best Local Similarity 63.2%; Pred. No. 7.2e+02;
Matches 12; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
```

```
QY      1 ATAAAAAGCTTCTTCACA 19
        ||| ||| ||| ||| |||
Db       1 AUAACAGCUCUCCACAUA 19
```

RESULT 22

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US-11-101-244-164932
; Sequence 164932, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 164932
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-164932
```

```
Query Match          71.0%; Score 14.2; DB 10; Length 19;
Best Local Similarity 63.2%; Pred. No. 7.2e+02;
Matches 12; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
```

```
QY      1 ATAAAAAGCTTCTTCACA 19
        ||| ||| ||| ||| |||
Db       1 AUAACAGCUCUCCACAUA 19
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RESULT 23

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US-11-101-244-289129
; Sequence 289129, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
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; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
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; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-289129
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Query Match          71.0%; Score 14.2; DB 10; Length 19;
Best Local Similarity 63.2%; Pred. No. 7.2e+02;
Matches 12; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
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```
QY      1 ATAAAAAGCTTCTTCACA 19
        ||| ||| ||| ||| |||
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RESULT 24

```
US-11-101-244-440211/C
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; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
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; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-440211
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Best Local Similarity 84.2%; Pred. No. 7.2e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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        ||| ||| ||| ||| |||
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RESULT 25

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; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
```


;; TITLE OF INVENTION: FOR GENETIC TRAITS AND VERIFYING PARENTAGE OF CANINE ANIMALS
;; FILE REFERENCE: MM1120-4
;; CURRENT APPLICATION NUMBER: US/10/972,767
;; CURRENT FILING DATE: 2004-10-25
;; PRIOR APPLICATION NUMBER: US 60/617,383
;; PRIOR FILING DATE: 2004-10-08
;; PRIOR APPLICATION NUMBER: US 60/514,180
;; PRIOR FILING DATE: 2003-10-24
;; NUMBER OF SEQ ID NOS: 404
;; SOFTWARE: PatentIn version 3.3
;; SEQ ID NO 48
;; LENGTH: 61
;; TYPE: DNA
;; ORGANISM: Artificial sequence
;; FEATURE:
;; OTHER INFORMATION: Amplification primer
US-10-972-767-48

Query Match 72.0%; Score 14.4; DB 7; Length 61;
Best Local Similarity 93.8%; Pred. No. 8.1e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 AAAAGCTTCTCAACA 19
DB 55 AAAAGCTTCTCAACA 40

RESULT 18
US-10-310-914A-1063031
;; Sequence 1063031, Application US/10310914A
;; Publication No. US20060003322A1
;; GENERAL INFORMATION:
;; APPLICANT: Bentwich, Isaac
;; APPLICANT: Shlier, Kiyazat
;; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
;; FILE REFERENCE: 06087.0200.CPUS01
;; CURRENT APPLICATION NUMBER: US/10/310,914A
;; CURRENT FILING DATE: 2002-12-06
;; NUMBER OF SEQ ID NOS: 1388402
;; SOFTWARE: PatentIn version 3.3
;; SEQ ID NO 1063031
;; LENGTH: 19
;; TYPE: RNA
;; ORGANISM: Human
US-10-310-914A-1063031

Query Match 71.0%; Score 14.2; DB 8; Length 19;
Best Local Similarity 63.2%; Pred. No. 7.2e+02;
Matches 12; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 2 TAAAAAGCTTCTCAAC 20
DB 1 UAAAAAGCTTCTCAAC 19

RESULT 19
US-11-101-244-164632
;; Sequence 164632, Application US/11101244
;; Publication No. US20050246794A1
;; GENERAL INFORMATION:
;; APPLICANT: Dharmoon, Inc.
;; APPLICANT: Khvorova, Anastasia
;; APPLICANT: Reynolds, Angela
;; APPLICANT: Leake, Devin
;; APPLICANT: Marshall, William
;; APPLICANT: Scaringe, Stephen
;; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
;; FILE REFERENCE: 13499US
;; CURRENT APPLICATION NUMBER: US/11/101,244
;; CURRENT FILING DATE: 2005-04-07
;; PRIOR APPLICATION NUMBER: 60/502,050
;; PRIOR FILING DATE: 2003-09-10

;; PRIOR APPLICATION NUMBER: 60/426,137
;; PRIOR FILING DATE: 2002-11-14
;; NUMBER OF SEQ ID NOS: 1591911
;; SOFTWARE: Proprietary
;; SEQ ID NO 164632
;; LENGTH: 19
;; TYPE: RNA
;; ORGANISM: Homo sapiens
US-11-101-244-164632

Query Match 71.0%; Score 14.2; DB 10; Length 19;
Best Local Similarity 63.2%; Pred. No. 7.2e+02;
Matches 12; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 ATAAAAAGCTTCTCAACA 19
DB 1 AAAAAAGCTTCTCAACA 19

RESULT 20
US-11-101-244-164732
;; Sequence 164732, Application US/11101244
;; Publication No. US20050246794A1
;; GENERAL INFORMATION:
;; APPLICANT: Dharmoon, Inc.
;; APPLICANT: Khvorova, Anastasia
;; APPLICANT: Reynolds, Angela
;; APPLICANT: Leake, Devin
;; APPLICANT: Marshall, William
;; APPLICANT: Scaringe, Stephen
;; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
;; FILE REFERENCE: 13499US
;; CURRENT APPLICATION NUMBER: US/11/101,244
;; CURRENT FILING DATE: 2005-04-07
;; PRIOR APPLICATION NUMBER: 60/502,050
;; PRIOR FILING DATE: 2003-09-10
;; PRIOR APPLICATION NUMBER: 60/426,137
;; PRIOR FILING DATE: 2002-11-14
;; NUMBER OF SEQ ID NOS: 1591911
;; SOFTWARE: Proprietary
;; SEQ ID NO 164732
;; LENGTH: 19
;; TYPE: RNA
;; ORGANISM: Homo sapiens
US-11-101-244-164732

Query Match 71.0%; Score 14.2; DB 10; Length 19;
Best Local Similarity 63.2%; Pred. No. 7.2e+02;
Matches 12; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 ATAAAAAGCTTCTCAACA 19
DB 1 AAAAAAGCTTCTCAACA 19

RESULT 21
US-11-101-244-164831
;; Sequence 164831, Application US/11101244
;; Publication No. US20050246794A1
;; GENERAL INFORMATION:
;; APPLICANT: Dharmoon, Inc.
;; APPLICANT: Khvorova, Anastasia
;; APPLICANT: Reynolds, Angela
;; APPLICANT: Leake, Devin
;; APPLICANT: Marshall, William
;; APPLICANT: Scaringe, Stephen
;; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
;; FILE REFERENCE: 13499US
;; CURRENT APPLICATION NUMBER: US/11/101,244
;; CURRENT FILING DATE: 2005-04-07
;; PRIOR APPLICATION NUMBER: 60/502,050
;; PRIOR FILING DATE: 2003-09-10
;; PRIOR APPLICATION NUMBER: 60/426,137

;; PRIOR APPLICATION NUMBER: US 60/585,352
;; PRIOR FILING DATE: 2004-07-02
;; NUMBER OF SEQ ID NOS: 116251
;; SOFTWARE: PatentIn version 3.2
;; SEQ ID NO 21315
;; LENGTH: 50
;; TYPE: DNA
;; ORGANISM: homo sapiens
US-11-175-859-21315

Query Match 74.0%; Score 14.8; DB 12; Length 50;
Best Local Similarity 80.0%; Pred. No. 4.7e+02;
Matches 16; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ATAAAGCTTCTCAACAC 20
Db 35 ATAAAAATCKTCTCCAATAC 16

RESULT 14
US-11-101-244-559589
;; Sequence 559589, Application US/11101244
;; Publication No. US20050246794A1
;; GENERAL INFORMATION:
;; APPLICANT: Dharmacon, Inc.
;; APPLICANT: Khvorova, Anastasia
;; APPLICANT: Reynolds, Angela
;; APPLICANT: Leake, Devin
;; APPLICANT: Marshall, William
;; APPLICANT: Scaringe, Stephen
;; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
;; FILE REFERENCE: 13499US
;; CURRENT APPLICATION NUMBER: US/11/101,244
;; PRIOR FILING DATE: 2005-04-07
;; PRIOR APPLICATION NUMBER: 60/502,050
;; PRIOR FILING DATE: 2003-09-10
;; PRIOR APPLICATION NUMBER: 60/426,137
;; PRIOR FILING DATE: 2002-11-14
;; NUMBER OF SEQ ID NOS: 1591911
;; SOFTWARE: Proprietary
;; SEQ ID NO 559589
;; LENGTH: 19
;; TYPE: RNA
;; ORGANISM: Homo sapiens
US-11-101-244-559589

Query Match 72.0%; Score 14.4; DB 10; Length 19;
Best Local Similarity 75.0%; Pred. No. 5.7e+02;
Matches 12; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 5 AAAGCTTCTCAACAC 20
Db 2 AAAGCCUCUCCACAC 17

RESULT 15
US-11-083-784-559589
;; Sequence 559589, Application US/11083784
;; Publication No. US20050245475A1
;; GENERAL INFORMATION:
;; APPLICANT: Dharmacon, Inc.
;; APPLICANT: Khvorova, Anastasia
;; APPLICANT: Reynolds, Angela
;; APPLICANT: Leake, Devin
;; APPLICANT: Marshall, William
;; APPLICANT: Scaringe, Stephen
;; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
;; FILE REFERENCE: 13499US
;; CURRENT APPLICATION NUMBER: US/11/083,784
;; PRIOR FILING DATE: 2005-03-18
;; PRIOR APPLICATION NUMBER: US/10/714,333
;; PRIOR FILING DATE: 2003-11-14
;; PRIOR APPLICATION NUMBER: 60/502,050

;; PRIOR FILING DATE: 2003-09-10
;; PRIOR APPLICATION NUMBER: 60/426,137
;; PRIOR FILING DATE: 2002-11-14
;; NUMBER OF SEQ ID NOS: 1591911
;; SOFTWARE: Proprietary
;; SEQ ID NO 559589
;; LENGTH: 19
;; TYPE: RNA
;; ORGANISM: Homo sapiens
US-11-083-784-559589

Query Match 72.0%; Score 14.4; DB 11; Length 19;
Best Local Similarity 75.0%; Pred. No. 5.7e+02;
Matches 12; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 5 AAAGCTTCTCAACAC 20
Db 2 AAAGCCUCUCCACAC 17

RESULT 16
US-10-972-767-351/C
;; Sequence 351, Application US/10972767
;; Publication No. US2006008815A1
;; GENERAL INFORMATION:
;; APPLICANT: METAMORPHIX, INC.
;; APPLICANT: Rosenfeld, David
;; APPLICANT: Kerr, Richard
;; APPLICANT: Hutton, Michelle
;; APPLICANT: Denise, Sue
;; APPLICANT: Bates, Stephen
;; APPLICANT: Fantin, Dennis
;; TITLE OF INVENTION: COMPOSITIONS, METHODS, AND SYSTEMS FOR INFERRING CANINE BREEDS
;; FILE REFERENCE: MM1120-4
;; CURRENT APPLICATION NUMBER: US/10/972,767
;; PRIOR FILING DATE: 2004-10-25
;; PRIOR APPLICATION NUMBER: US 60/617,383
;; PRIOR FILING DATE: 2004-10-08
;; PRIOR APPLICATION NUMBER: US 60/514,180
;; PRIOR FILING DATE: 2003-10-24
;; NUMBER OF SEQ ID NOS: 404
;; SOFTWARE: PatentIn version 3.3
;; SEQ ID NO 351
;; LENGTH: 25
;; TYPE: DNA
;; ORGANISM: Artificial sequence
;; FEATURE:
;; OTHER INFORMATION: Amplification Primer
US-10-972-767-351

Query Match 72.0%; Score 14.4; DB 7; Length 25;
Best Local Similarity 93.8%; Pred. No. 6.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 AAAAGCTTCTCAACA 19
Db 20 AAAAGCTTCTCAACA 5

RESULT 17
US-10-972-767-48/C
;; Sequence 48, Application US/10972767
;; Publication No. US2006008815A1
;; GENERAL INFORMATION:
;; APPLICANT: METAMORPHIX, INC.
;; APPLICANT: Rosenfeld, David
;; APPLICANT: Kerr, Richard
;; APPLICANT: Hutton, Michelle
;; APPLICANT: Denise, Sue
;; APPLICANT: Bates, Stephen
;; APPLICANT: Fantin, Dennis
;; TITLE OF INVENTION: COMPOSITIONS, METHODS, AND SYSTEMS FOR INFERRING CANINE BREEDS

ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: Probe
US-11-136-527-291020

Query Match 76.0%; Score 15.2; DB 12; Length 25;
Best Local Similarity 85.0%; Pred. No. 2.4e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ATAAAGCTTCTTCAACAC 20
|||||:|||||:
Db 5 ATAAATCTTCTTCACTC 24

RESULT 9
US-11-136-527-291028
Sequence 291028, Application US/11136527
Publication No. US20050287570A1
GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Mounts, William M
TITLE OF INVENTION: Probe Arrays for Expression Profiling of Rat Genes
FILE REFERENCE: 031896-041000 (AM101086)
CURRENT APPLICATION NUMBER: US/11/136,527
CURRENT FILING DATE: 2005-05-25
PRIOR APPLICATION NUMBER: US 60/574,294
PRIOR FILING DATE: 2005-05-26
NUMBER OF SEQ ID NOS: 362830
SOFTWARE: PatentIn version 3.2
SEQ ID NO 291028
LENGTH: 25
TYPE: DNA
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: Probe
US-11-136-527-291028

Query Match 76.0%; Score 15.2; DB 12; Length 25;
Best Local Similarity 85.0%; Pred. No. 2.4e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ATAAAGCTTCTTCAACAC 20
|||||:|||||:
Db 1 ATAAATCTTCTTCACTC 20

RESULT 10
US-11-175-859-32149
Sequence 32149, Application US/11175859
Publication No. US20060024715A1
GENERAL INFORMATION:
APPLICANT: Affymetrix, Inc.
APPLICANT: Liu, Guoying et al.
TITLE OF INVENTION: Method of Analysis of Human Polymorphism
FILE REFERENCE: 3690.1
CURRENT APPLICATION NUMBER: US/11/175,859
CURRENT FILING DATE: 2005-07-05
PRIOR APPLICATION NUMBER: US 60/585,352
PRIOR FILING DATE: 2004-07-02
NUMBER OF SEQ ID NOS: 116251
SOFTWARE: PatentIn version 3.2
SEQ ID NO 32149
LENGTH: 50
TYPE: DNA
ORGANISM: homo sapien
US-11-175-859-32149

Query Match 75.0%; Score 15; DB 12; Length 50;
Best Local Similarity 88.2%; Pred. No. 3.7e+02;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ATAAAGCTTCTTCAAC 17
|||||:|||||:

Db 21 ATAAAGCTTCTTCAAC 37

RESULT 11
US-10-310-914A-345949
Sequence 345949, Application US/10310914A
Publication No. US20060003322A1
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Shiller, Kvazut
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
FILE REFERENCE: 06087.0200 CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
SEQ ID NO 345949
LENGTH: 19
TYPE: RNA
ORGANISM: Human
US-10-310-914A-345949

Query Match 74.0%; Score 14.8; DB 8; Length 19;
Best Local Similarity 66.7%; Pred. No. 3.6e+02;
Matches 12; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ATAAAGCTTCTTCAAC 18
|||||:|||||:
Db 1 AAAAAAAAAAATCTTCAAC 18

RESULT 12
US-11-175-859-4340/c
Sequence 4340, Application US/11175859
Publication No. US20060024715A1
GENERAL INFORMATION:
APPLICANT: Affymetrix, Inc.
APPLICANT: Liu, Guoying et al.
TITLE OF INVENTION: Method of Analysis of Human Polymorphism
FILE REFERENCE: 3690.1
CURRENT APPLICATION NUMBER: US/11/175,859
CURRENT FILING DATE: 2005-07-05
PRIOR APPLICATION NUMBER: US 60/585,352
PRIOR FILING DATE: 2004-07-02
NUMBER OF SEQ ID NOS: 116251
SOFTWARE: PatentIn version 3.2
SEQ ID NO 4340
LENGTH: 50
TYPE: DNA
ORGANISM: homo sapien
US-11-175-859-4340

Query Match 74.0%; Score 14.8; DB 12; Length 50;
Best Local Similarity 80.0%; Pred. No. 4.7e+02;
Matches 16; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ATAAAGCTTCTTCAACAC 20
|||||:|||||:
Db 35 ATAAATCTTCTTCACTC 16

RESULT 13
US-11-175-859-21315/c
Sequence 21315, Application US/11175859
Publication No. US20060024715A1
GENERAL INFORMATION:
APPLICANT: Affymetrix, Inc.
APPLICANT: Liu, Guoying et al.
TITLE OF INVENTION: Method of Analysis of Human Polymorphism
FILE REFERENCE: 3690.1
CURRENT APPLICATION NUMBER: US/11/175,859
CURRENT FILING DATE: 2005-07-05

Db 13 ATCAAGAGCTTCTCAACA 31

RESULT 4

US-11-121-849-284248
; Sequence 284248, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; TITLE OF INVENTION: Microarrays
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 284248
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-284248

Query Match 77.0%; Score 15.4; DB 12; Length 25;
Best Local Similarity 94.1%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 AAAAGCTTCTTCAACAC 20
Db 1 AAAAGCTTCTTCAACGC 17

RESULT 5

US-11-121-849-113350
; Sequence 113350, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; TITLE OF INVENTION: Microarrays
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 113350
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-113350

Query Match 76.0%; Score 15.2; DB 12; Length 25;
Best Local Similarity 85.0%; Pred. No. 2.4e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ATAAAAAGCTTCTTCAACAC 20
Db 3 ATAAATAAGCTACTTGAACAC 22

RESULT 6

US-11-136-527-290998
; Sequence 290998, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)

; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 290998
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Probe
US-11-136-527-290998

Query Match 76.0%; Score 15.2; DB 12; Length 25;
Best Local Similarity 85.0%; Pred. No. 2.4e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ATAAAAAGCTTCTTCAACAC 20
Db 4 ATAAATAATCTTCTCAGCTC 23

RESULT 7

US-11-136-527-291008
; Sequence 291008, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 291008
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Probe
US-11-136-527-291008

Query Match 76.0%; Score 15.2; DB 12; Length 25;
Best Local Similarity 85.0%; Pred. No. 2.4e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ATAAAAAGCTTCTTCAACAC 20
Db 3 ATAAATAATCTTCTCAGCTC 22

RESULT 8

US-11-136-527-291020
; Sequence 291020, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 291020
; LENGTH: 25
; TYPE: DNA

94 13.4 67.0 19 10 US-11-101-244-1276075 Sequence 1276075,
95 13.4 67.0 19 11 US-11-083-784-45882 Sequence 45882, A
96 13.4 67.0 19 11 US-11-083-784-35584 Sequence 35584, A
97 13.4 67.0 19 11 US-11-083-784-35584 Sequence 35584, A
98 13.4 67.0 19 11 US-11-083-784-356702 Sequence 356702,
99 13.4 67.0 19 11 US-11-083-784-559605 Sequence 559605,
100 13.4 67.0 19 11 US-11-083-784-609758 Sequence 609758,
100 13.4 67.0 19 11 US-11-083-784-609839 Sequence 609839,

ALIGNMENTS

RESULT 1
US-10-923-476A-254/c
Sequence 254, Application US/10923476A
Publication No. US20050288242A1
GENERAL INFORMATION:
APPLICANT: Sina Therapeutics, Inc.
TITLE OF INVENTION: RNA Interference Mediated Inhibition Of RAS Gene Expression Using
FILE REFERENCE: 400/231 (MBH01-1158-B)
CURRENT FILING DATE: 2004-08-20
CURRENT FILING DATE: 2004-08-20
PRIOR APPLICATION NUMBER: US 10/238,700
PRIOR FILING DATE: 2002-09-10
PRIOR APPLICATION NUMBER: PCT/US02/16840
PRIOR FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: 60/318,471
PRIOR FILING DATE: 2001-09-10
PRIOR APPLICATION NUMBER: PCT/US04/16390
PRIOR FILING DATE: 2004-05-24
PRIOR APPLICATION NUMBER: US 10/826,966
PRIOR FILING DATE: 2004-04-16
PRIOR APPLICATION NUMBER: US 10/757,803
PRIOR FILING DATE: 2004-01-14
PRIOR APPLICATION NUMBER: US 10/720,448
PRIOR FILING DATE: 2003-11-24
PRIOR APPLICATION NUMBER: US 10/693,059
PRIOR FILING DATE: 2003-10-23
PRIOR APPLICATION NUMBER: US 10/444,853
PRIOR FILING DATE: 2003-05-23
PRIOR APPLICATION NUMBER: PCT/US03/05346
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 766
SOFTWARE: Patentin version 3.3
SEQ ID NO 254
LENGTH: 19
TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic
US-10-923-476A-254
Query Match 87.0%; Score 17.4; DB 8; Length 19;
Best Local Similarity 94.7%; Pred. No. 16;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2 TAAAGCTTCTTCAACAC 20
DB 19 TAAAGCATCTTCAACAC 1
RESULT 2
US-10-923-476A-363
Sequence 363, Application US/10923476A
Publication No. US20050288242A1
GENERAL INFORMATION:
APPLICANT: Sina Therapeutics, Inc.
TITLE OF INVENTION: RNA Interference Mediated Inhibition Of RAS Gene Expression Using
FILE REFERENCE: 400/231 (MBH01-1158-B)
CURRENT FILING DATE: 2004-08-20
CURRENT FILING DATE: 2004-08-20
PRIOR APPLICATION NUMBER: US 10/238,700
PRIOR FILING DATE: 2002-09-10
PRIOR APPLICATION NUMBER: PCT/US02/16840
PRIOR FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: 60/318,471
PRIOR FILING DATE: 2001-09-10
PRIOR APPLICATION NUMBER: PCT/US04/16390
PRIOR FILING DATE: 2004-05-24
PRIOR APPLICATION NUMBER: US 10/826,966
PRIOR FILING DATE: 2004-04-16
PRIOR APPLICATION NUMBER: US 10/757,803
PRIOR FILING DATE: 2004-01-14
PRIOR APPLICATION NUMBER: US 10/720,448
PRIOR FILING DATE: 2003-11-24
PRIOR APPLICATION NUMBER: US 10/693,059
PRIOR FILING DATE: 2003-10-23
PRIOR APPLICATION NUMBER: US 10/444,853
PRIOR FILING DATE: 2003-05-23
PRIOR APPLICATION NUMBER: PCT/US03/05346
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 766
SOFTWARE: Patentin version 3.3
SEQ ID NO 363
LENGTH: 19
TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic
US-10-923-476A-363
Query Match 87.0%; Score 17.4; DB 8; Length 19;
Best Local Similarity 73.7%; Pred. No. 16;
Matches 14; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
QY 2 TAAAGCTTCTTCAACAC 20
DB 1 UAAAGCAUCUUCACAC 19
RESULT 3
US-10-630-154-31
Sequence 31, Application US/10630154
Publication No. US20060040268A1
GENERAL INFORMATION:
APPLICANT: McCreedy, Paula M
APPLICANT: Radnedge, Lynsey
APPLICANT: Anderson, Gary L
APPLICANT: Ott, Linda L
APPLICANT: Slezak, Thomas R
APPLICANT: Kuczmarski, Thomas A
APPLICANT: Vitale, Elizabeth A
TITLE OF INVENTION: Nucleotide Sequences Specific to Francisella Tularensis and
FILE REFERENCE: IL-11031
CURRENT FILING DATE: US/10/630,154
CURRENT FILING DATE: 2003-07-29
NUMBER OF SEQ ID NOS: 32
SOFTWARE: Patentin version 3.2
SEQ ID NO 31
LENGTH: 33
TYPE: DNA
ORGANISM: Francisella tularensis
US-10-630-154-31
Query Match 79.0%; Score 15.8; DB 7; Length 33;
Best Local Similarity 89.5%; Pred. No. 1.3e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 ATAAAGCTTCTTCAACA 19

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: March 1, 2006, 22:45:50 ; Search time 496 Seconds
(without alignments)
88.402 Million cell updates/sec

Title: US-10-653-528-32
Perfect score: 20
Sequence: 1 ataaagctcttcaacac 20

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 7218512 seqs, 1096188070 residues

Total number of hits satisfying chosen parameters: 11869650

Minimum DB seq length: 0
Maximum DB seq length: 80

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database :

Published Applications NA_New:*
1: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
2: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
4: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
5: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
6: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq1:*
7: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq1:*
8: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq1:*
9: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq2:*
10: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq3:*
11: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq4:*
12: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq4:*
13: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	17.4	87.0	19 8	US-10-923-476A-254	Sequence 254, App
2	17.4	87.0	19 8	US-10-923-476A-363	Sequence 363, App
3	15.8	79.0	33 7	US-10-630-154-31	Sequence 31, Appl
4	15.4	77.0	25 12	US-11-121-849-284248	Sequence 284248,
5	15.2	76.0	25 12	US-11-121-849-113350	Sequence 113350,
6	15.2	76.0	25 12	US-11-136-527-290998	Sequence 290998,
7	15.2	76.0	25 12	US-11-136-527-291008	Sequence 291008,
8	15.2	76.0	25 12	US-11-136-527-291020	Sequence 291020,
9	15.2	76.0	25 12	US-11-136-527-291028	Sequence 291028,
10	15	75.0	50 12	US-11-175-859-33149	Sequence 33149, A
11	14.8	74.0	19 8	US-10-310-914A-345949	Sequence 345949, A
12	14.8	74.0	50 12	US-11-175-859-4340	Sequence 4340, Ap
C 13	14.8	74.0	50 12	US-11-175-859-21315	Sequence 21315, A
14	14.4	72.0	19 10	US-11-101-244-559589	Sequence 559589,
15	14.4	72.0	19 11	US-11-083-784-559589	Sequence 559589,
C 16	14.4	72.0	25 7	US-10-972-767-351	Sequence 351, App
C 17	14.4	72.0	61 7	US-10-972-767-48	Sequence 48, Appl
18	14.2	71.0	19 8	US-10-310-914A-1603031	Sequence 1603031,
19	14.2	71.0	19 10	US-11-101-244-164632	Sequence 164632,
20	14.2	71.0	19 10	US-11-101-244-164732	Sequence 164732,

21	14.2	71.0	19 10	US-11-101-244-164831	Sequence 164831,
22	14.2	71.0	19 10	US-11-101-244-164932	Sequence 164932,
23	14.2	71.0	19 10	US-11-101-244-289129	Sequence 289129,
C 24	14.2	71.0	19 10	US-11-101-244-440211	Sequence 440211,
25	14.2	71.0	19 10	US-11-101-244-453541	Sequence 453541,
C 26	14.2	71.0	19 10	US-11-101-244-572442	Sequence 572442,
27	14.2	71.0	19 11	US-11-083-784-164632	Sequence 164632,
28	14.2	71.0	19 11	US-11-083-784-164732	Sequence 164732,
29	14.2	71.0	19 11	US-11-083-784-164831	Sequence 164831,
30	14.2	71.0	19 11	US-11-083-784-164932	Sequence 164932,
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C 32	14.2	71.0	19 11	US-11-083-784-440211	Sequence 440211,
C 33	14.2	71.0	19 11	US-11-083-784-453541	Sequence 453541,
C 34	14.2	71.0	19 11	US-11-083-784-572442	Sequence 572442,
C 35	14.2	71.0	22 8	US-10-310-914A-118116	Sequence 118116,
C 36	14.2	71.0	50 12	US-11-175-859-35895	Sequence 35895, A
C 37	14.2	71.0	50 12	US-11-175-859-104157	Sequence 104157,
38	14	70.0	50 12	US-11-175-859-75311	Sequence 75311, A
C 39	14	70.0	50 12	US-11-175-859-106126	Sequence 106126,
C 40	13.8	69.0	19 8	US-10-310-914A-208187	Sequence 208187,
C 41	13.8	69.0	19 10	US-11-101-244-45896	Sequence 45896, A
C 42	13.8	69.0	19 10	US-11-101-244-313427	Sequence 313427,
C 43	13.8	69.0	19 10	US-11-101-244-637850	Sequence 637850,
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45	13.8	69.0	19 10	US-11-101-244-1349359	Sequence 1349359,
C 46	13.8	69.0	19 11	US-11-083-784-45896	Sequence 45896, A
C 47	13.8	69.0	19 11	US-11-083-784-313427	Sequence 313427,
C 48	13.8	69.0	19 11	US-11-083-784-637850	Sequence 637850,
49	13.8	69.0	19 11	US-11-083-784-1349355	Sequence 1349355,
50	13.8	69.0	19 11	US-11-083-784-1349359	Sequence 1349359,
51	13.8	69.0	20 8	US-10-310-914A-1079636	Sequence 1079636,
C 52	13.8	69.0	21 8	US-10-310-914A-66405	Sequence 66405, A
C 53	13.8	69.0	21 8	US-10-310-914A-168329	Sequence 168329,
C 54	13.8	69.0	23 8	US-10-310-914A-960384	Sequence 960384,
55	13.8	69.0	24 8	US-10-310-914A-1070874	Sequence 1070874,
56	13.8	69.0	24 8	US-10-310-914A-1368375	Sequence 1368375,
C 57	13.8	69.0	25 8	US-10-775-169-1758	Sequence 1758, Ap
58	13.8	69.0	25 8	US-10-310-914A-199616	Sequence 199616,
59	13.8	69.0	25 8	US-10-310-914A-1037846	Sequence 1037846,
60	13.8	69.0	25 12	US-11-121-849-74838	Sequence 74838, A
61	13.8	69.0	25 12	US-11-121-849-74839	Sequence 74839, A
62	13.8	69.0	25 12	US-11-121-849-74840	Sequence 74840, A
63	13.8	69.0	25 12	US-11-121-849-128912	Sequence 128912,
C 64	13.8	69.0	25 12	US-11-175-859-5715	Sequence 5715, Ap
65	13.8	69.0	50 12	US-11-175-859-43318	Sequence 43318, A
66	13.8	69.0	50 12	US-11-175-859-80650	Sequence 80650, A
C 67	13.8	69.0	23 8	US-10-310-914A-861643	Sequence 861643,
68	13.6	68.0	25 12	US-11-121-849-144901	Sequence 144901,
69	13.6	68.0	25 12	US-11-121-849-569174	Sequence 569174,
C 70	13.6	68.0	25 12	US-11-121-849-665969	Sequence 665969,
71	13.6	68.0	25 12	US-11-136-527-106886	Sequence 106886,
72	13.6	68.0	27 12	US-11-010-954-10	Sequence 10, Appl
C 73	13.6	68.0	27 12	US-11-053-750-10	Sequence 10, Appl
74	13.6	68.0	27 12	US-11-053-750-10	Sequence 10, Appl
C 75	13.6	68.0	27 12	US-11-170-753-10	Sequence 10, Appl
76	13.6	68.0	27 12	US-11-181-030-10	Sequence 10, Appl
77	13.6	68.0	27 12	US-11-181-030-10	Sequence 10, Appl
78	13.6	68.0	27 12	US-11-181-030-10	Sequence 10, Appl
79	13.6	68.0	27 12	US-11-181-030-10	Sequence 10, Appl
80	13.6	68.0	27 12	US-11-181-030-10	Sequence 10, Appl
81	13.6	68.0	27 12	US-11-181-030-10	Sequence 10, Appl
82	13.6	68.0	50 12	US-11-175-859-24499	Sequence 24499, A
C 83	13.4	67.0	19 10	US-11-101-244-45882	Sequence 45882, A
C 84	13.4	67.0	19 10	US-11-101-244-355584	Sequence 355584,
C 85	13.4	67.0	19 10	US-11-101-244-356702	Sequence 356702,
C 86	13.4	67.0	19 10	US-11-101-244-559605	Sequence 559605,
C 87	13.4	67.0	19 10	US-11-101-244-609839	Sequence 609839,
C 88	13.4	67.0	19 10	US-11-101-244-609857	Sequence 609857,
C 89	13.4	67.0	19 10	US-11-101-244-609874	Sequence 609874,
C 90	13.4	67.0	19 10	US-11-101-244-685293	Sequence 685293,
C 91	13.4	67.0	19 10	US-11-101-244-685300	Sequence 685300,
C 92	13.4	67.0	19 10	US-11-101-244-685367	Sequence 685367,
C 93	13.4	67.0	19 10	US-11-101-244-696108	Sequence 696108,

Qy 1 ATAAAGCTTCTCAACA 19
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 Db 24 ATAAATCGTCATCAACA 6

RESULT 30

US-10-843-527-210555
 ; Sequence 210555, Application US/10843527
 ; Publication No. US20050136395A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Michael Miltmann
 ; APPLICANT: Eric Schell
 ; TITLE OF INVENTION: Methods of Genetic Analysis of SARS Virus
 ; FILE REFERENCE: 3602.1
 ; CURRENT APPLICATION NUMBER: US/10/843,527
 ; PRIOR FILING DATE: 2004-05-10
 ; PRIOR APPLICATION NUMBER: 60/469,545
 ; NUMBER OF SEQ ID NOS: 238196
 ; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
 ; SEQ ID NO 210555
 ; LENGTH: 25
 ; TYPE: DNA
 ; ORGANISM: SARS Virus
 ; US-10-843-527-210555

Query Match 71.0%; Score 14.2; DB 9; Length 25;
 Best Local Similarity 84.2%; Pred. No. 1.4e+04;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ATAAAGCTTCTCAACA 19
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 Db 2 ATAAATCGTCATCAACA 20

Search completed: March 1, 2006, 23:22:48
 Job time : 619.333 secs

Db 19 TAGAAGCTTCTGAACC 1

RESULT 25

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; Sequence 259791, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mount, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 259791
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-259791

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Query Match 71.0%; Score 14.2; DB 9; Length 25;
 Best Local Similarity 84.2%; Pred. No. 1.4e+04;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 TAAAAAGCTTCTTCACAC 20
 Db 19 TAGAAGCTTCTGAACC 1

RESULT 26

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; Sequence 26645, Application US/10843527
; Publication No. US20050136395A1
; GENERAL INFORMATION:
; APPLICANT: Michael Miltmann
; APPLICANT: Eric Schell
; TITLE OF INVENTION: Methods of Genetic Analysis of SARS Virus
; FILE REFERENCE: 3602.1
; CURRENT APPLICATION NUMBER: US/10/843,527
; CURRENT FILING DATE: 2004-05-10
; PRIOR APPLICATION NUMBER: 60/469,545
; PRIOR FILING DATE: 2003-05-08
; NUMBER OF SEQ ID NOS: 238196
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 26645
; LENGTH: 25
; TYPE: DNA
; ORGANISM: SARS Virus
US-10-843-527-26645

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Query Match 71.0%; Score 14.2; DB 9; Length 25;
 Best Local Similarity 84.2%; Pred. No. 1.4e+04;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ATAAAAAGCTTCTTCACAC 19
 Db 25 ATAAAAAGCTTCTTCACAC 7

RESULT 27

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; Sequence 26648, Application US/10843527
; Publication No. US20050136395A1
; GENERAL INFORMATION:
; APPLICANT: Michael Miltmann
; APPLICANT: Eric Schell
; TITLE OF INVENTION: Methods of Genetic Analysis of SARS Virus
; FILE REFERENCE: 3602.1
; CURRENT APPLICATION NUMBER: US/10/843,527
; CURRENT FILING DATE: 2004-05-10

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; PRIOR APPLICATION NUMBER: 60/469,545

; PRIOR FILING DATE: 2003-05-08

; NUMBER OF SEQ ID NOS: 238196

; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

; SEQ ID NO 26648

; LENGTH: 25

; TYPE: DNA

; ORGANISM: SARS Virus

US-10-843-527-26648

Query Match 71.0%; Score 14.2; DB 9; Length 25;
 Best Local Similarity 84.2%; Pred. No. 1.4e+04;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ATAAAAAGCTTCTTCACAC 19
 Db 22 ATAAAAAGCTTCTTCACAC 4

RESULT 28

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; Sequence 27138, Application US/10843527
; Publication No. US20050136395A1
; GENERAL INFORMATION:
; APPLICANT: Michael Miltmann
; APPLICANT: Eric Schell
; TITLE OF INVENTION: Methods of Genetic Analysis of SARS Virus
; FILE REFERENCE: 3602.1
; CURRENT APPLICATION NUMBER: US/10/843,527
; CURRENT FILING DATE: 2004-05-10
; PRIOR APPLICATION NUMBER: 60/469,545
; PRIOR FILING DATE: 2003-05-08
; NUMBER OF SEQ ID NOS: 238196
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 27138
; LENGTH: 25
; TYPE: DNA
; ORGANISM: SARS Virus
US-10-843-527-27138

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Query Match 71.0%; Score 14.2; DB 9; Length 25;
 Best Local Similarity 84.2%; Pred. No. 1.4e+04;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ATAAAAAGCTTCTTCACAC 19
 Db 20 ATAAAAAGCTTCTTCACAC 2

RESULT 29

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; Sequence 27622, Application US/10843527
; Publication No. US20050136395A1
; GENERAL INFORMATION:
; APPLICANT: Michael Miltmann
; APPLICANT: Eric Schell
; TITLE OF INVENTION: Methods of Genetic Analysis of SARS Virus
; FILE REFERENCE: 3602.1
; CURRENT APPLICATION NUMBER: US/10/843,527
; CURRENT FILING DATE: 2004-05-10
; PRIOR APPLICATION NUMBER: 60/469,545
; PRIOR FILING DATE: 2003-05-08
; NUMBER OF SEQ ID NOS: 238196
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 27622
; LENGTH: 25
; TYPE: DNA
; ORGANISM: SARS Virus
US-10-843-527-27622

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Query Match 71.0%; Score 14.2; DB 9; Length 25;
 Best Local Similarity 84.2%; Pred. No. 1.4e+04;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db 25 TCAAAAGCTTCTACACAC 7

RESULT 20
US-10-719-956-403149
; Sequence 403149, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002.11.20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 403149
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-403149

Query Match 71.0%; Score 14.2; DB 7; Length 25;
Best Local Similarity 84.2%; Pred. No. 1.4e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ATAAAAGCTTCTTCACAC 19
Db 6 AGAAACAGCTTCTCCACCA 24

RESULT 21
US-10-719-900-559116/c
; Sequence 559116, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002.11.20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 559116
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-559116

Query Match 71.0%; Score 14.2; DB 8; Length 25;
Best Local Similarity 84.2%; Pred. No. 1.4e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ATAAAAGCTTCTTCACAC 19
Db 25 ATAAACAGCTTCTATACAC 7

RESULT 22
US-10-719-900-613240/c
; Sequence 613240, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808

; PRIOR FILING DATE: 2002.11.20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 613240
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-613240

Query Match 71.0%; Score 14.2; DB 8; Length 25;
Best Local Similarity 84.2%; Pred. No. 1.4e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ATAAAAGCTTCTTCACAC 19
Db 23 ATAAAAGCTTCTGACACCA 5

RESULT 23
US-10-956-157-227840
; Sequence 227840, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 227840
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-227840

Query Match 71.0%; Score 14.2; DB 9; Length 25;
Best Local Similarity 84.2%; Pred. No. 1.4e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ATAAAAGCTTCTTCACAC 19
Db 4 ATAAAGAGCTTCTGCACGA 22

RESULT 24
US-10-956-157-259790/c
; Sequence 259790, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 259790
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-259790

Query Match 71.0%; Score 14.2; DB 9; Length 25;
Best Local Similarity 84.2%; Pred. No. 1.4e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TAAAAGCTTCTTCACAC 20
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;; CURRENT APPLICATION NUMBER: US/10/719,956
;; CURRENT FILING DATE: 2003-11-20
;; PRIOR APPLICATION NUMBER: 60/427,836
;; PRIOR FILING DATE: 2002-11-20
;; NUMBER OF SEQ ID NOS: 699466
;; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
;; SEQ ID NO 681188
;; LENGTH: 25
;; TYPE: DNA
;; ORGANISM: Rattus norvegicus
US-10-719-956-681188

Query Match 72.0%; Score 14.4; DB 7; Length 25;
Best Local Similarity 93.8%; Pred. No. 1.1e+04;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 AAAAGCTCTTCAACA 19
Db 6 AAAAGCTCTTCAACA 21

RESULT 16
US-11-036-317-96728/c
; Sequence 96728, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 96728
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-96728

Query Match 72.0%; Score 14.4; DB 10; Length 25;
Best Local Similarity 93.8%; Pred. No. 1.1e+04;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 AAAAGCTCTTCAACA 19
Db 17 AAATGCTTCTTCAACA 2

RESULT 17
US-10-640-968A-6
; Sequence 6, Application US/10640968A
; Publication No. US20040224414A1
; GENERAL INFORMATION:
; APPLICANT: Julien, Bryan
; TITLE OF INVENTION: TRANSPOSON-BASED TRANSFORMATION SYSTEM
; FILE REFERENCE: 300622009800
; CURRENT APPLICATION NUMBER: US/10/640,968A
; CURRENT FILING DATE: 2003-08-13
; PRIOR APPLICATION NUMBER: US 60/403,290
; PRIOR FILING DATE: 2002-08-13
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 33
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-640-968A-6

Query Match 72.0%; Score 14.4; DB 8; Length 33;
Best Local Similarity 93.8%; Pred. No. 1.2e+04;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 AAAAGCTCTTCAACA 19
Db 1 AAAAGCTTATTCACA 16

RESULT 18
US-10-714-161-31/c
; Sequence 31, Application US/10714161
; Publication No. US20050026825A1
; GENERAL INFORMATION:
; APPLICANT: Carlton, Mark
; APPLICANT: Aparicio, Samuel
; APPLICANT: Dixon, John
; APPLICANT: Thresher, Rosemary
; APPLICANT: Zahn, Dirk
; TITLE OF INVENTION: Receptor
; FILE REFERENCE: 674580-2004
; CURRENT APPLICATION NUMBER: US/10/714,161
; CURRENT FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: PCT/GB02/02304
; PRIOR FILING DATE: 2002-05-16
; PRIOR APPLICATION NUMBER: GB 011959.3
; PRIOR FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: US 60/292,141
; PRIOR FILING DATE: 2001-05-18
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 31
; LENGTH: 42
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-10-714-161-31

Query Match 72.0%; Score 14.4; DB 8; Length 42;
Best Local Similarity 93.8%; Pred. No. 1.3e+04;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ATAAAAAGCTTCTCA 16
Db 41 ATAAAAAGCTTCTCA 26

RESULT 19
US-10-719-956-79762/c
; Sequence 79762, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 79762
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-79762

Query Match 71.0%; Score 14.2; DB 7; Length 25;
Best Local Similarity 84.2%; Pred. No. 1.4e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 TAAAAAGCTCTTCAACAC 20

ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Oligonucleotide
US-10-220-481-169

Query Match 76.0%: Score 15.2; DB 7; Length 33;
Best Local Similarity 85.0%: Pred. No. 5.2e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ATAAAGCTTCTTCAACAC 20
|||
Db 13 ATGAAAGCTTCTTCAAAAC 32

RESULT 11
US-10-098-263B-118837
; Sequence 118837, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Miltman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 118837
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-118837

Query Match 74.0%: Score 14.8; DB 5; Length 25;
Best Local Similarity 88.9%: Pred. No. 7.5e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 AAAAAGCTTCTTCAACAC 20
|||
Db 2 AAAAAGCTTCTTCAAGAC 19

RESULT 12
US-10-098-263B-118838
; Sequence 118838, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Miltman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 118838
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-118838

Query Match 74.0%: Score 14.8; DB 5; Length 25;
Best Local Similarity 88.9%: Pred. No. 7.5e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 AAAAAGCTTCTTCAACAC 20
|||
Db 2 AAAAAGCTTCTTCAAGAC 19

RESULT 13

US-11-036-317-859238
; Sequence 859238, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 859238
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-859238

Query Match 74.0%: Score 14.8; DB 10; Length 25;
Best Local Similarity 88.9%: Pred. No. 7.5e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 AAAAAGCTTCTTCAACAC 20
|||
Db 1 AATAAGCTTCTTCAACAC 18

RESULT 14
US-10-339-767-9
; Sequence 9, Application US/10339767
; Publication No. US20030207301A1
; GENERAL INFORMATION:
; APPLICANT: GMP Endotherapeutics, Inc.
; APPLICANT: Taylor-Fishwick, David A
; APPLICANT: Vinik, Aaron I
; TITLE OF INVENTION: Assay for the Detection of Factors that Modulate the Expression
; FILE REFERENCE: 9061X.HLS
; CURRENT APPLICATION NUMBER: US/10/339,767
; CURRENT FILING DATE: 2003-01-09
; PRIOR APPLICATION NUMBER: US 60/388,315
; PRIOR FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: US 60/361,073
; PRIOR FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 60/346,898
; PRIOR FILING DATE: 2002-01-11
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Hamster sp.
US-10-339-767-9

Query Match 72.0%: Score 14.4; DB 6; Length 22;
Best Local Similarity 93.8%: Pred. No. 1.1e+04;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 AAAAAGCTTCTTCAAC 18
|||
Db 7 AAAAAGCTTCTTCAAC 22

RESULT 15
US-10-719-956-681188
; Sequence 681188, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1

US-10-653-528-43

Query Match 85.0%; Score 17; DB 7; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.4e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 AAAAGCTTCTTCAACAC 20
Db 1 AAAAGCTTCTTCAACAC 17

RESULT 6

US-10-653-528-67/c
; Sequence 67, Application US/10653528
; Publication No. US2004007578A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 2 EXPRESSION
; FILE REFERENCE: PFS-0022
; CURRENT APPLICATION NUMBER: US/10/653,528
; CURRENT FILING DATE: 2003-09-02
; PRIOR APPLICATION NUMBER: US/10/173,192
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 71
; SEQ ID NO 67
; LENGTH: 20
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
US-10-653-528-67

Query Match 85.0%; Score 17; DB 7; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.4e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 AAAAGCTTCTTCAACAC 20
Db 20 AAAAGCTTCTTCAACAC 4

RESULT 7

US-10-719-956-79761/c
; Sequence 79761, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 79761
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-79761

Query Match 79.0%; Score 15.8; DB 7; Length 25;
Best Local Similarity 89.5%; Pred. No. 2.7e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TAAAAAGCTTCTTCAACAC 20
Db 25 TCAAAAGCTTCTTCAACAC 7

RESULT 8

US-10-956-157-227426/c
; Sequence 227426, Application US/10956157

; Publication No. US20050118625A1

; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 227426
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-227426

Query Match 76.0%; Score 15.2; DB 9; Length 25;
Best Local Similarity 85.0%; Pred. No. 5e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ATAAAAAGCTTCTTCAACAC 20
Db 24 ATAAAAAGCTTCTTCAACAC 5

RESULT 9

US-11-036-317-964784
; Sequence 964784, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 964784
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-964784

Query Match 76.0%; Score 15.2; DB 10; Length 25;
Best Local Similarity 85.0%; Pred. No. 5e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ATAAAAAGCTTCTTCAACAC 20
Db 2 ATAAAAAGCTTCTTCAACAC 21

RESULT 10

US-10-220-481-169
; Sequence 169, Application US/10220481
; Publication No. US20040110670A1
; GENERAL INFORMATION:
; APPLICANT: ARICO, Maria B., et al.
; TITLE OF INVENTION: Heterologous Expression of Neisserial Proteins
; FILE REFERENCE: CHIR-15883/0105
; CURRENT APPLICATION NUMBER: US/10/220,481
; CURRENT FILING DATE: 2003-05-05
; PRIOR APPLICATION NUMBER: PCT/IB01/00452
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 633
; SOFTWARE: SeqMan9, version 1.02
; SEQ ID NO 169
; LENGTH: 33
; TYPE: DNA

97 13.6 68.0 27 6 US-10-379-866-10 Sequence 10, Appl
98 13.6 68.0 27 6 US-10-371-962-10 Sequence 10, Appl
99 13.6 68.0 27 7 US-10-665-971-10 Sequence 10, Appl
100 13.6 68.0 27 7 US-10-637-759-10 Sequence 10, Appl

ALIGNMENTS

RESULT 1

US-10-173-192-32
; Sequence 32, Application US/10173192
; Publication No. US20030236204A1
; GENERAL INFORMATION:
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 2 EXPRESSION
; FILE REFERENCE: PTS-0022
; CURRENT APPLICATION NUMBER: US/10/173,192
; CURRENT FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 71
; SEQ ID NO 32
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-173-192-32

Query Match 100.0%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATAAAGCTTCTTCAACAC 20
Db 1 ATAAAGCTTCTTCAACAC 20

RESULT 2

US-10-653-528-32
; Sequence 32, Application US/10653528
; Publication No. US2004007578A1
; GENERAL INFORMATION:
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 2 EXPRESSION
; FILE REFERENCE: PTS-0022
; CURRENT APPLICATION NUMBER: US/10/653,528
; CURRENT FILING DATE: 2003-09-02
; PRIOR APPLICATION NUMBER: US/10/173,192
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 71
; SEQ ID NO 32
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-653-528-32

Query Match 100.0%; Score 20; DB 7; Length 20;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATAAAGCTTCTTCAACAC 20
Db 1 ATAAAGCTTCTTCAACAC 20

RESULT 3

US-10-173-192-43
; Sequence 43, Application US/10173192
; Publication No. US20030236204A1

; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 2 EXPRESSION
; FILE REFERENCE: PTS-0022
; CURRENT APPLICATION NUMBER: US/10/173,192
; CURRENT FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 71
; SEQ ID NO 43
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-173-192-43

Query Match 85.0%; Score 17; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 7,4e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 AAAAGCTTCTTCAACAC 20
Db 1 AAAAGCTTCTTCAACAC 17

RESULT 4

US-10-173-192-67/c
; Sequence 67, Application US/10173192
; Publication No. US20030236204A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 2 EXPRESSION
; FILE REFERENCE: PTS-0022
; CURRENT APPLICATION NUMBER: US/10/173,192
; CURRENT FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 71
; SEQ ID NO 67
; LENGTH: 20
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
US-10-173-192-67

Query Match 85.0%; Score 17; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 7,4e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 AAAAGCTTCTTCAACAC 20
Db 20 AAAAGCTTCTTCAACAC 4

RESULT 5

US-10-653-528-43
; Sequence 43, Application US/10653528
; Publication No. US2004007578A1
; GENERAL INFORMATION:
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 2 EXPRESSION
; FILE REFERENCE: PTS-0022
; CURRENT APPLICATION NUMBER: US/10/653,528
; CURRENT FILING DATE: 2003-09-02
; PRIOR APPLICATION NUMBER: US/10/173,192
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 71
; SEQ ID NO 43
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: March 1, 2006, 22:34:29 ; Search time 617.333 Seconds

(without alignments)
267.906 Million cell updates/sec

Title: US-10-653-528-32
Perfect score: 20
Sequence: 1 ataaaagctcttcaacac 20

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 413468905 residues

Total number of hits satisfying chosen parameters: 11282798

Minimum DB seq length: 0
Maximum DB seq length: 80

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database :

Published Applications_NA_Main:*

- 1: /cgn2_6/prodata/1/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/prodata/1/pubpna/US08_PUBCOMB.seq:*
- 3: /cgn2_6/prodata/1/pubpna/US09A_PUBCOMB.seq:*
- 4: /cgn2_6/prodata/1/pubpna/US09B_PUBCOMB.seq:*
- 5: /cgn2_6/prodata/1/pubpna/US10A_PUBCOMB.seq:*
- 6: /cgn2_6/prodata/1/pubpna/US10B_PUBCOMB.seq:*
- 7: /cgn2_6/prodata/1/pubpna/US10C_PUBCOMB.seq:*
- 8: /cgn2_6/prodata/1/pubpna/US10E_PUBCOMB.seq:*
- 9: /cgn2_6/prodata/1/pubpna/US10F_PUBCOMB.seq:*
- 10: /cgn2_6/prodata/1/pubpna/US11_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	* Query Match Length	DB ID	Description
1	20	100.0	20 6 US-10-173-192-32	Sequence 32, Appl
2	20	100.0	20 7 US-10-653-528-32	Sequence 43, Appl
3	17	85.0	20 6 US-10-173-192-43	Sequence 43, Appl
4	17	85.0	20 6 US-10-173-192-67	Sequence 67, Appl
5	17	85.0	20 7 US-10-653-528-67	Sequence 43, Appl
6	17	85.0	20 7 US-10-653-528-67	Sequence 67, Appl
7	15.8	79.0	25 9 US-10-956-157-227426	Sequence 79761, A
8	15.2	76.0	25 9 US-10-956-157-227426	Sequence 227426, A
9	15.2	76.0	25 10 US-11-036-317-964784	Sequence 964784, A
10	15.2	76.0	33 7 US-10-220-481-169	Sequence 169, App
11	14.8	74.0	25 5 US-10-098-2638-118837	Sequence 118837, A
12	14.8	74.0	25 5 US-10-098-2638-118838	Sequence 118838, A
13	14.8	74.0	25 10 US-11-036-317-859238	Sequence 859238, A
14	14.4	72.0	22 6 US-10-339-767-9	Sequence 9, Appl
15	14.4	72.0	25 7 US-10-719-956-681188	Sequence 681188, A
16	14.4	72.0	25 10 US-11-036-317-96728	Sequence 96728, A
17	14.4	72.0	33 8 US-10-640-968A-6	Sequence 6, Appl
18	14.4	72.0	42 8 US-10-714-161-31	Sequence 31, Appl
19	14.2	71.0	25 7 US-10-719-956-79762	Sequence 79762, A
20	14.2	71.0	25 7 US-10-719-956-403149	Sequence 403149, A
21	14.2	71.0	25 8 US-10-719-900-559116	Sequence 559116, A
22	14.2	71.0	25 8 US-10-719-900-613240	Sequence 613240, A
23	14.2	71.0	25 9 US-10-956-157-227840	Sequence 227840, A

C 24	14.2	71.0	25 9 US-10-956-157-259790	Sequence 259790, A
C 25	14.2	71.0	25 9 US-10-956-157-259791	Sequence 259791, A
C 26	14.2	71.0	25 9 US-10-843-527-26648	Sequence 26648, A
C 27	14.2	71.0	25 9 US-10-843-527-26648	Sequence 26648, A
C 28	14.2	71.0	25 9 US-10-843-527-27138	Sequence 27138, A
C 29	14.2	71.0	25 9 US-10-843-527-27622	Sequence 27622, A
C 30	14.2	71.0	25 9 US-10-843-527-210555	Sequence 210555, A
C 31	14.2	71.0	25 9 US-10-843-527-211039	Sequence 211039, A
C 32	14.2	71.0	25 9 US-10-843-527-211529	Sequence 211529, A
C 33	14.2	71.0	25 9 US-10-843-527-211532	Sequence 211532, A
C 34	14.2	71.0	25 10 US-11-036-317-962406	Sequence 962406, A
C 35	14.2	71.0	29 6 US-10-353-174-21	Sequence 21, Appl
C 36	14.2	71.0	29 10 US-11-006-372-21	Sequence 21, Appl
C 37	14.2	71.0	42 8 US-10-828-924-12	Sequence 12, Appl
C 38	14.2	71.0	47 6 US-10-170-097-1230	Sequence 1230, Ap
C 39	14.2	71.0	47 8 US-10-926-684-1230	Sequence 1230, Ap
C 40	14.2	71.0	60 3 US-09-008-975-13839	Sequence 13839, A
C 41	14	70.0	20 6 US-10-173-192-24	Sequence 24, Appl
C 42	14	70.0	20 6 US-10-173-192-24	Sequence 24, Appl
C 43	14	70.0	20 7 US-10-653-528-24	Sequence 24, Appl
C 44	14	70.0	20 7 US-10-653-528-24	Sequence 24, Appl
C 45	14	70.0	25 10 US-11-060-756-213651	Sequence 213651, A
C 46	13.8	69.0	17 3 US-09-730-2898-186	Sequence 186, App
C 47	13.8	69.0	20 6 US-10-094-749-3375	Sequence 3375, Ap
C 48	13.8	69.0	24 9 US-10-625-755-998	Sequence 998, App
C 49	13.8	69.0	24 9 US-10-470-0738-998	Sequence 998, App
C 50	13.8	69.0	25 5 US-10-098-2638-106755	Sequence 106755, A
C 51	13.8	69.0	25 7 US-10-719-956-22037	Sequence 22037, Ap
C 52	13.8	69.0	25 7 US-10-719-956-102511	Sequence 102511, A
C 53	13.8	69.0	25 7 US-10-719-956-292906	Sequence 292906, A
C 54	13.8	69.0	25 7 US-10-719-956-351169	Sequence 351169, A
C 55	13.8	69.0	25 8 US-10-719-956-390323	Sequence 390323, A
C 56	13.8	69.0	25 8 US-10-775-169-1758	Sequence 1758, Ap
C 57	13.8	69.0	25 8 US-10-719-900-598973	Sequence 598973, A
C 58	13.8	69.0	25 8 US-10-719-900-654663	Sequence 654663, A
C 59	13.8	69.0	25 10 US-11-036-317-798753	Sequence 798753, A
C 60	13.8	69.0	60 3 US-09-908-975-3197	Sequence 3197, Ap
C 61	13.8	69.0	65 6 US-10-032-585-3197	Sequence 3197, Ap
C 62	13.8	69.0	79 3 US-09-788-590-12192	Sequence 12192, A
C 63	13.8	69.0	24 9 US-10-625-755-989	Sequence 989, App
C 64	13.6	68.0	24 9 US-10-470-0738-989	Sequence 989, App
C 65	13.6	68.0	25 7 US-10-719-956-93967	Sequence 93967, A
C 66	13.6	68.0	25 8 US-10-719-900-216124	Sequence 216124, A
C 67	13.6	68.0	25 8 US-10-719-900-612449	Sequence 612449, A
C 68	13.6	68.0	25 8 US-10-719-900-720754	Sequence 720754, A
C 69	13.6	68.0	25 9 US-10-809-189-117345	Sequence 117345, A
C 70	13.6	68.0	25 10 US-11-036-317-6598	Sequence 6598, Ap
C 71	13.6	68.0	25 10 US-11-036-317-773816	Sequence 773816, A
C 72	13.6	68.0	25 10 US-11-036-317-955497	Sequence 955497, A
C 73	13.6	68.0	25 10 US-11-036-317-959893	Sequence 959893, A
C 74	13.6	68.0	25 10 US-11-036-317-959893	Sequence 959893, A
C 75	13.6	68.0	25 10 US-11-036-317-959893	Sequence 959893, A
C 76	13.6	68.0	25 10 US-11-036-317-959893	Sequence 959893, A
C 77	13.6	68.0	25 10 US-11-036-317-959893	Sequence 959893, A
C 78	13.6	68.0	27 3 US-09-756-301A-10	Sequence 286710, A
C 79	13.6	68.0	27 3 US-09-756-301A-10	Sequence 286710, A
C 80	13.6	68.0	27 3 US-09-756-301A-10	Sequence 286710, A
C 81	13.6	68.0	27 3 US-09-756-301A-10	Sequence 286710, A
C 82	13.6	68.0	27 3 US-09-756-301A-10	Sequence 286710, A
C 83	13.6	68.0	27 3 US-09-756-301A-10	Sequence 286710, A
C 84	13.6	68.0	27 3 US-09-756-301A-10	Sequence 286710, A
C 85	13.6	68.0	27 3 US-09-756-301A-10	Sequence 286710, A
C 86	13.6	68.0	27 3 US-09-756-301A-10	Sequence 286710, A
C 87	13.6	68.0	27 3 US-09-756-301A-10	Sequence 286710, A
C 88	13.6	68.0	27 3 US-09-756-301A-10	Sequence 286710, A
C 89	13.6	68.0	27 3 US-09-756-301A-10	Sequence 286710, A
C 90	13.6	68.0	27 3 US-09-756-301A-10	Sequence 286710, A
C 91	13.6	68.0	27 3 US-09-756-301A-10	Sequence 286710, A
C 92	13.6	68.0	27 3 US-09-756-301A-10	Sequence 286710, A
C 93	13.6	68.0	27 3 US-09-756-301A-10	Sequence 286710, A
C 94	13.6	68.0	27 3 US-09-756-301A-10	Sequence 286710, A
C 95	13.6	68.0	27 3 US-09-756-301A-10	Sequence 286710, A
C 96	13.6	68.0	27 3 US-09-756-301A-10	Sequence 286710, A